

This sequence represents the *S. pyogenes* plasmin receptor. The DNA encoding this sequence was isolated from the *S. pyogenes* clinical isolate 64/14. The Plasmin receptor has a very high affinity for plasmin which, when bound, retains its enzymatic activity but is not regulated (inhibited) by alpha-2-antiplasmin. The receptor protein, when administered concurrently or sequentially, prolongs the activity of plasminogen activator (PA) so allows a reduction in dose, and thus lowers the risk of bleeding, and may prevent reocclusion of blood vessels. The protein may be coupled to a fibrin-specific monoclonal antibody to provide targeting to clots. The plasmin receptor may be useful in human or veterinary medicine, for treatment of thrombosis and pulmonary embolism, and for solubilising clots in catheters or shunts. (Updated on 25-MAR-2003 to correct P field)

Sequence 336 AA:

Query Match Best Local Similarity Score 1711; DB 2; Length 336;

1 MVVKVYINGFGRIGRLAARRRIONVEGVEVTRINLTDPNMLAHLLKYDTTQGR
1 MNGFCYTGNGFCYTGNGFCYTGNGFCYTGNGFCYTGNGFCYTGNGFCYTGNGFCYTG

61 KEGGGFEVNGNFIVKUSAERDPENIDPNTATDGEIVLEATGFFAKKEAEKHLHAN

61 KEGG PENGNIKSAERDSENIDATBGEIVLEATGFARKEAEERLHAN 121

121 TAPGGNDVKTVVFNTNHDILDGTETVISGASCITNCIAPMAKALHDAFGIQKG

181 YTGDQM:LDGPHRGGLRRARAGAANTVPNSTGAAKAIIGLVIPELNGKLDGAA

241 GSVTELVYTLDKNVSYDEINAAMKAASNDSFGYTEDPIVSSDIVGVSYGSLFDD

241 GSVTELVITLDKNUVSDEINSAMKAASNDSGYTEDPIVSSDIVGVSYGSLFD.

301 EVDGSQLVKKVSYWDNEMSYTAQLVRTLEYFAKIAK 336

ISSUE 7

~~AAU85681~~ AAY85681 standard; protein; 336 AA.

13-FEB-2001 (First entry)
Anjouan,

Streptococcal plasmin receptor amino acid sequence.

rasmin receptor, pII, immune response; vaccination; adicabac Streptococcal infection; antihelminthic.

streptococcus *pyogenes*.
US6136323-A

24-OCT-2000.

11-JUL-1994; 9408S-0002732247.
29-MAR-1989; 8903300849

16-MAY-1990; 900US-000524411.
10-AUG-1992; 920US-000928462.

(U2FL) UNIV FLORIDA RES FOUND INC.

PI	Von Mering G,	Broder C,	Lotterberg R,	Boyle MDP;
XX	WPI: 2001-006210/01.			
DR	N PSDB; AAC66140.			
XX	Raising an immune response in a mammal, especially against group A streptococcal infections, comprises isolated streptococcal Plasmin receptor protein.			
PT	Claim 2; Col 27-30; 17PP; English.			
XX	Polynucleotide sequence AAC66140 encodes the Streptococcal receptor protein AAY65681. The protein is used in a mammal. The method comprises a Plasmin receptor protein. The method is useful as a group A Streptococcal infections and potentially against pathogens expressing glycoprotein hydrolyase (GAPDH) or GAPDH-like proteins. The vaccine has antibacterial and antibacterial surfaces.			
PS	Sequence 336 AA;			
XX	Query Match 99.8%; Score 1711; DB 4; Leucine 2; Mismatches 0; I			
XX	Best Local Similarity 99.4%; Pred. No. 2e 144;			
XX	Matches 334; Conservative 2; Mismatches 0; I			
Qy	1 MVTKVGTNGFGRIGRLAFRRIQNEVGEVTRINDLTDPMNLAA			
Db	1 MVTKVGTNGFGRIGRLAFRRIQNEVGEVTRINDLTDPMNLAA			
Qy	61 KEGCFEYGNFIVKSAERPDENDWATDGVETIVLEATGPFPAK			
Db	61 KEGCFEYGNFIVKSAERPDENDWATDGVETIVLEATGPFPAK			
Qy	121 TAPCGNDVYKTVVFTNTNHDLDGTEVTISGASCTINCLAPAK			
Db	121 TAGGNDVYKTVVFTNTNHDLDGTEVTISGASCTINCLAPAK			
Qy	181 YTGQMDLGDGHGGDLRRAGAAGANIVPNSTGAAKAGIIVI			
Db	181 YTGQMDLGDGHGGDLRRAGAAGANIVPNSTGAAKAGIIVI			
Qy	241 GSTTELVYTLDRNSVDEINSAKGAASNSFGTTEDPVSSD			
Db	241 GSTTELVYTLDRNSVDEINSAKGAASNSFGTTEDPVSSD			
Qy	301 EVDGSQLYKVSVYDNEMSYTAQLVRTLEYFAKIAK 336			
Db	301 EVDGSQLYKVSVYDNEMSYTAQLVRTLEYFAKIAK 336			
RESULT 8				
	AAM50664			
ID	AAM50664 standard; protein; 448 AA.			
XX	XX			
AC	AC			
XX	XX			
DT	29-AUG-2003 (revised)			
DT	08-APR-2002 (first entry)			
DE	Streptococcus GapC multiepitope fusion PolyGap4.			
XX	PolyGap4; GapC; Plasmin binding protein; epitope; immunisation; mastitis; therapy.			
XX	Streptococcus dysgalactiae.			
OS	Streptococcus agalactiae.			
OS	Streptococcus parauberis.			
XX	Chimeric.			
OS	WC000196379-A2.			
XX	PN			
PD	20-DEC-2001.			

XX 11-JUN-2001; 2001WO-CA000836.
 PF XX
 PR 12-JUN-2000; 2000US-0211247P.
 PA (USA-) UNIV SASKATCHEWAN.
 XX
 PI Porter AA, Perez-Casal J, Fontaine M;
 XX
 DR WPI; 2002-098051/13.
 N-PSDB; ABA91327.
 XX
 PS Novel GAPC multiple epitope fusion polypeptide comprising antigenic determinants of Streptococcus dysgalactiae, S. agalactiae, S. uberis, S. parauensis, or S. iniae GAPC protein useful for treating mastitis in vertebrates.
 XX
 CC Claim 9; Fig 6A-C; 116PP; English.
 CC The present sequence is that of a novel multiple epitope fusion protein, designated PolyGAP4, comprising the entire amino acid sequence of the Streptococcus dysgalactiae GAPC plasmin binding protein in addition to unique amino acid sequences from the Streptococcus parauensis and Streptococcus agalactiae GAPC proteins. The multiple epitope protein is produced in host cells transformed with an expression vector comprising a chimeric gene (see ABA91327) encoding the protein. PolyGAP4 is an example of novel GAPC multiple epitope fusion proteins of the invention that can comprise epitopes from 1 or more of S. dysgalactiae, S. agalactiae, S. parauensis, Streptococcus uberis and Streptococcus iniae (see AAM5065-69). The multiple epitope fusion proteins are used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection, and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope protein is capable of eliciting broad immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 Sequence 448 AA;
 SQ Query Match 96.6%; Score 1656.5; DB 5; Length 448;
 Best Local Similarity 79.6%; Pred. No. 2.2e-139; Mismatches 0; Gaps 1;
 Matches 339; Conservative 0; Gaps 1; Indels 85; Gaps 1;
 CC The present sequence is that of the GAPC plasmin binding protein, ÜberGAPC, of Streptococcus uberis ATCC 9927. The invention relates to ÜberGAPC, of Streptococcus uberis ATCC 9927. The invention relates to ÜberGAPC, of Streptococcus uberis ATCC 9927. The invention relates to ÜberGAPC, of Streptococcus agalactiae, Streptococcus dysgalactiae, Streptococcus parauensis, Streptococcus iniae or more of Streptococcus dysgalactiae, Streptococcus parauensis, Streptococcus iniae or more of Streptococcus dysgalactiae, Streptococcus parauensis, Streptococcus iniae (see AAM5065-69). A claimed example is PolyGAP4 (see AAM5065-69).
 CC Expression vectors and host cells for production of the multiple epitope fusion proteins are provided. The multiple epitope proteins are used in claimed vaccines for treating or preventing a bacterial infection in a vertebrate, especially a streptococcal infection, and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope proteins are capable of eliciting broad immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs
 XX
 PS Fig 3A-B; 116PP; English.
 XX
 CC The present sequence is that of the GAPC plasmin binding protein, ÜberGAPC, of Streptococcus uberis ATCC 9927. The invention relates to ÜberGAPC, of Streptococcus agalactiae, Streptococcus dysgalactiae, Streptococcus parauensis, Streptococcus iniae or more of Streptococcus dysgalactiae, Streptococcus parauensis, Streptococcus iniae (see AAM5065-69). A claimed example is PolyGAP4 (see AAM5065-69).
 CC Expression vectors and host cells for production of the multiple epitope fusion proteins are provided. The multiple epitope proteins are used in claimed vaccines for treating or preventing a bacterial infection, and particularly mastitis. They are also used in claimed methods of detecting Streptococcus antibodies. The multiple epitope proteins are capable of eliciting broad immunity against a variety of streptococcal infections while minimising the number of antigens present in the final formulation and concomitantly reducing production costs
 XX
 PS Sequence 336 AA;
 SQ Query Match 94.3%; Score 1618; DB 5; Length 336;
 Best Local Similarity 92.9%; Pred. No. 4.1e-136; Mismatches 9; Gaps 0;
 Matches 312; Conservative 15; Gaps 0;
 CC 1 MVVKVINGGRIGRIGLAFRIGRIONYEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDTVEV 60
 28 MVVKVINGGRIGRIGLAFRIGRIONYEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDTVEV 87
 61 KEGGEFVNGFIKVSÄERDE----- 81
 88 KEGGEFVNGFIKVSÄERDEBENIDWATDGVIVLEALEGTVVEKDGFDVNGKPKVSAE 147
 82 -----NIDWATDGVIVLE-----NIDWATDGVIVLE 95
 148 KDPEQIDWATDGVIVLEIDGTVVEKGGFPEVNGOFVKVSAEREPANIDWATDGVIVLE 207
 96 ATGFFAKKEAEEKHLHANGAKKVVITAPGENDVYKTVVFNTNHDILDGTETVSGASCTTN 155
 208 ATSFAKKEAEEKHLHANGAKKVVITAPGENDVYKTVVFNTNHDILDGTETVSGASCTTN 267
 156 CLAPNAKALFADFQTKGMLTIIAYTGDONILDGPGRGDLRRAAGANIVPNSTGAA 215
 268 CLAPNAKALFADFQTKGMLTIIAYTGDONILDGPGRGDLRRAAGANIVPNSTGAA 327
 216 KAIGLVIPELNGKLDDAAQRVPVPGPSVTEVLTIVTLDKNSVDEINAAMKASNSDFGYTE 275
 328 KAIGLVIPELNGKLDDAAQRVPVPGPSVTEVLTIVTLDKNSVDEINAAMKASNSDFGYTE 387
 276 DPIVSSDIVGYSYGSILPDATAQTKMVEYDGSQVVKVTSWYNEMSYTAQLVRTLEYFAKA 335
 388 DPIVSSDIVGYSYGSILPDATAQTKMVEYDGSQVVKVTSWYNEMSYTAQLVRTLEYFAKA 447
 CC 1 MVVKVINGGRIGRIGLAFRIGRIONYEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDTVEV 60
 1 MVVKVINGGRIGRIGLAFRIGRIONYEGVEVTRINDLTDPNMLAHLLKYDTTQGRFDTVEV 60
 61 KEGGFVNGFIKVSÄERDEBENIDWATDGVIVLEALEGTVVEKDGFDVNGKPKVSAE 120
 61 KDGGEFVNGFIKVSÄERDEBENIDWATDGVIVLE-----NIDWATDGVIVLE 120
 121 TAPGENDVYKTVVFNTNHDILDGTETVSGASCTTN 180

Db 121 TAPGDDVKTIVVENTNHDIDGTEVITISGASCTNCLAPMAKALQDNFCVKQGILMTIHA 180
 Qy 181 YTGDOMILDGHRGGDLRARRAGANTIPNSTGAAKAAIGLIVIPELNGKLDGAACRVPVT 240
 Db 181 YTGDOMILDGHRGGDLRARRAGANTIPNSTGAAKAAIGLIVIPELNGKLDGAACRVPVT 240
 Db 181 YTGDOMILDGHRGGDLRARRAGANTIPNSTGAAKAAIGLIVIPELNGKLDGAACRVPVT 240
 Qy 241 GSVTELVVTIDKNSVDEINAMKAANDSGYTEDPIVSSDIVGVSYGSLSFDATOTKVM 300
 Db 241 GSVTELVVTIDKNSVDEINAMKAANDSGYTEDPIVSSDIVGVSYGSLSFDATOTKVM 300
 Qy 301 EVDGSQLVKTVSWYDNEMSYTAQLVRLTEYPAKIAK 336
 Db 301 TVDGNQLVKTVSWYDNEMSYTAQLVRLTEYPAKIAK 336
 RESULT 10
 AAM50641 standard; protein; 336 AA.
 ID AAM50641
 AC AAM50641;
 XX DT 04-APR-2002 (first entry)
 DE Streptococcus uberis gapC plasmin binding protein.
 XX KW Plasmin-binding protein; UberGapC; infection; mastitis; vaccine;
 XX diagnosis; therapy.
 OS Streptococcus uberis.
 XX WO200196381-A2.
 PN 20-DEC-2001.
 PD 11-JUN-2001; 2001WO-CA000838.
 PR 12-JUN-2000; 2000US-0211022P.
 XX (UYSA-) UNIV SASKATCHEWAN.
 PA PI Bolton AJ, Perez-Casaj J, Fontaine M, Potter AA;
 XX DR WPI: 2002-130725/17.
 XX DR- N-PSDB; ABA91250.
 PT Novel isolated GapC protein of Streptococcus dysgalactiae, *S. agalactiae*,
 PT *S. uberis*, *S. parauensis*, or *S. iniae*, useful as vaccine component for
 PT treating streptococcal infection which causes mastitis in vertebrates.
 XX
 PS Claim 1(c); Fig 3A-B; 10pp; English.
 XX
 CC The present sequence is that of the GapC plasmin binding protein
 CC (*UberGapC*) of *Streptococcus uberis* ATCC 9927, encoded by the GapC gene
 CC given in ABA1250. GapC, which has no signal sequence or membrane anchor
 CC domain, is capable of eliciting an immune response in a vertebrate. The
 CC invention provides the GapC genes and proteins of 5 *Streptococcus*
 CC species, as well as recombinant vectors, host cells and vaccine
 CC compositions comprising GapC polynucleotides or proteins. The vaccines
 CC are used to treat or prevent a bacterial infection, especially a
 CC streptococcal infection, and mastitis in particular (claimed) GapC
 CC proteins are also used in claimed methods for detecting GapC antibodies,
 CC and to raise antibodies that are used in claimed methods for detecting
 CC GapC proteins. *S. uberis* is a common pathogen associated with mastitis in
 CC cattle, horse, sheep and goat
 XX Sequence 336 AA;
 SC Query Match 94.3%; Score 1618; DB 5; Length 336;
 CC Best Local Similarity 92.9%; Pred. No. 4.1e-136;
 CC Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 CC 1 MYVKVGINGFGRIGRLAARRRIONVEGVEVTRINDLTDPMNLALHLLRTDTQGRFDGVTEV 60
 CC Nucleic acids encoding (I) are used to detect *Streptococcus* in a

Db 61 KEGGFYEVNGNFIKVSAERDPENIDWATDGYBIVLEATGFFAKKEAEBKHLHANGAKKVV 120
 Qy 61 KDGGEVNGNFIKVSAERDPENIDWATDGYBIVLEATGFFAKKEAEBKHLHANGAKKVV 120
 Db 121 TA PGDDYKTVFVENTHDLIDGTEVITISGASCTNCLAPMAKALQDNFCVKQGILMTIHA 180
 Qy 121 TA PGDDYKTVFVENTHDLIDGTEVITISGASCTNCLAPMAKALQDNFCVKQGILMTIHA 180
 Db 121 TA PGDDYKTVFVENTHDLIDGTEVITISGASCTNCLAPMAKALQDNFCVKQGILMTIHA 180
 Qy 181 YTGDQMLDGPHRGDLRARRAGANTIPNSTGAAIGLIVIPELNGKLDGAACRVPVT 240
 Db 181 YTGDQMLDGPHRGDLRARRAGANTIPNSTGAAIGLIVIPELNGKLDGAACRVPVT 240
 Qy 241 GSVTELVVTIDKNSVDEINAMKAANDSGYTEDPIVSSDIVGVSYGSLSFDATOTKVM 300
 Qy 301 EVDGSQLVKTVSWYDNEMSYTAQLVRLTEYPAKIAK 336
 Db 301 TVDGNQLVKTVSWYDNEMSYTAQLVRLTEYPAKIAK 336
 RESULT 11
 ABP30758 standard; protein; 336 AA.
 ID ABP30758
 XX AC ABP30758;
 XX DT 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 10692.
 XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 XX group A streptococcus; Streptococcus pyogenes; antibiotic; antiinflammatory;
 XX infection; vaccine; meningitis; gene therapy.
 XX Streptococcus agalactiae.
 OS WO200234771-A2.
 XX PD 02-MAY-2002.
 XX PF 29-OCT-2001; 2001WO-GB004789.
 XX PR 27-OCT-2000; 2000GB-00026333.
 PR 24-NOV-2000; 2000GB-00028127.
 PR 07-MAR-2001; 2001GB-00005640.
 XX (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX PA WO200234771-A2.
 PI Telford J, Massignani V, Margarit Y Rost, Grandi G, Fraser C,
 PI Tellelin H,
 DR WPI: 2002-352536/38.
 DR N-PSDB; ABN1389.
 PT New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for
 PT detecting a compound that binds to the protein.
 XX
 CC Claim 1; Page 4179; 4525pp; English.
 CC
 CC The invention relates to a protein (ABP20895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes) comprising one of 9483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN604-ABN1526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly *S. agalactiae* and *S. pyogenes*.
 CC Nucleic acids encoding (I) are used to detect *Streptococcus* in a

CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 XX Streptococcus proteins

SQ Sequence 336 AA;

Query Match 93.8%; Score 1609; DB 5; Length 336;
 Best Local Similarity 92.0%; Pred. No. 2.6e-135; Mismatches 17; Indels 0; Gaps 0;
 Matches 309; Conservative 17; Gaps 0;

Qy 1 MVVKVGINGFGRIGLAFARRIQNVEGVETRINDLTDPNLALIILKYDITQGRDGIVTE 60
 Db 1 MVVKVGINGFGRIGLAFARRIQNVEGVETRINDLTDPNLALIILKYDITQGRDGIVTE 60
 Qy 61 KEGGPENNGNFTKVSAAERDPENIDWATDGVBIVLEATGFFAKKEAAEKHLHANGAKKVV 120
 Db 61 KEGGFENNGQFTKVSAAERPANIDWATDGVBIVLEATGFFAKKEAAEKHLHANGAKKVV 120

Qy 121 TAPGNDVKTVYTFNTNDILDCTETVSGASCTTCLAPMAKALHDAPGQKGLMTTHA 180
 Db 121 TAPGNDVKTVYTFNTNDILDCTETVSGASCTTCLAPMAKALQDNPGYKQKGLMTTHA 180

Qy 181 YTGDQMLIDGPHRGDILRARAAGANTVNSTGAAKAIGLVIPEINGKLGAAQRVPVFT 240
 Db 181 YTGDQMLIDGPHRGDILRARAAGANIVNSTGAAKAIGLVIPEINGKLGAAQRVPVFT 240

Qy 241 GSVTELYVTLDEKNSVYDEINAKMASNDSGYTEDPIVSSDIVEVSYSGLFDATQTKW 300
 Db 241 GSVTELYVTLDEKNSVYDEINAKMASNDSGYTEDPIVSSDIVEVSYSGLFDATQTKW 300

Qy 301 EVDGSOLVKVVSWYDNEMSYTAQLYRTLEYFAKIAK 336
 Db 301 TVDGNQLVKVVSWYDNEMSYTSQVLRTLEYFAKIAK 336

RESULT 12

AAM50666
 ID AAM50666 standard; protein; 336 AA.
 AC AAM50666;
 XX

DT 08-APR-2002 (first entry)

XX Streptococcus agalactiae gapC plasmin binding protein AgaGapC.
 KW AgaGapC; GapC; Plasmin binding protein; epitope; infection; vaccine;
 KW immunotherapy; mastitis; therapy.
 XX Streptococcus agalactiae.

XX OS AAM50640;
 XX PN AAM50640;
 XX DT 04-APR-2002 (first entry)

XX XX Streptococcus agalactiae gapC plasmin binding protein.
 DE XX
 KW XX
 Diagnosis; therapy.
 XX XX
 Streptococcus agalactiae.
 OS XX
 PN WO200196381-A2.
 DR XX
 DR 20-DEC-2001.
 PR XX
 PR 11-JUN-2001; 2001WO-CA0000836.
 PR XX
 PR 12-JUN-2000; 2000US-0211247P.
 PR XX
 PR (UYSA-) UNIV SASKATCHEWAN.
 PR XX
 PR Potter AA, Perez-Casal J, Fontaine M;
 PR XX
 PR WPI; 2002-098051-13.
 PR N-PSDB, ABA91329.
 PR XX
 PR Novel GapC multiple epitope fusion polypeptide comprising antigenic
 PR determinant of Streptococcus dysgalactiae, S. agalactiae, S. uberis, S.
 PR paruberis, or S. iniae GapC protein useful for treating mastitis in

PT vertebrates.
 XX Claim 8; Fig 2A-B; 116pp; English.
 PS
 XX
 CC The present sequence is that of the GapC plasmin binding protein.
 CC AgaGapC, of Streptococcus agalactiae ATCC 27541. The invention relates
 CC to novel GapC multiple epitope fusion proteins that comprise epitopes
 CC from 1 or more of Streptococcus dysgalactiae, Streptococcus agalactiae,
 CC Streptococcus paruberis, Streptococcus uberis, and Streptococcus iniae
 CC (see AAM50665-69). A claimed example is Polygap4 (see AAM50664).
 CC Expression vectors and host cells for production of the multiple epitope
 CC fusion proteins are provided. The multiple epitope proteins are used in
 CC claimed vaccines for treating or preventing a bacterial infection in a
 CC vertebrate, especially streptococcal infection, and particularly
 CC mastitis. They are also used in claimed methods of detecting
 CC Streptococcus antibodies. The multiple epitope proteins are capable of
 CC eliciting broad immunity against a variety of streptococcal infections
 CC while minimising the number of antigens present in the final formulation
 CC and concomitantly reducing production costs
 XX
 SQ Sequence 336 AA;
 Query Match 93.4%; Score 1602; DB 5; Length 336;
 Best Local Similarity 91.7%; Pred. No. 1.1e-134;
 Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MTKVGINGFGRIGLAFARRIQNVEGVETRINDLTDPNMIAHLIKYDITQGRFDGIVTE 60
 Db 1 MTKVGINGFGRIGLAFARRIQNVEGVETRINDLTDPNMIAHLIKYDITQGRFDGIVTE 60

Qy 61 KEGGFENNGNFTKVSAAERDPENIDWATDGVBIVLEATGFFAKKEAAEKHLHANGAKKVV 120
 Db 61 KEGGFENNGQFTKVSAAERPANIDWATDGVBIVLEATGFFAKKEAAEKHLHANGAKKVV 120

Qy 121 TAPGNDVKTVYTFNTNDILDCTETVSGASCTTCLAPMAKALHDAPGQKGLMTTHA 180
 Db 121 TAPGNDVKTVYTFNTNDILDCTETVSGASCTTCLAPMAKALQDNPGYKQKGLMTTHA 180

Qy 181 YTGDQMLIDGPHRGDILRARAAGANTVNSTGAAKAIGLVIPEINGKLGAAQRVPVFT 240
 Db 181 YTGDQMLIDGPHRGDILRARAAGANIVNSTGAAKAIGLVIPEINGKLGAAQRVPVFT 240

Qy 241 GSVTELYVTLDEKNSVYDEINAKMASNDSGYTEDPIVSSDIVEVSYSGLFDATQTKW 300
 Db 241 GSVTELYVTLDEKNSVYDEINAKMASNDSGYTEDPIVSSDIVEVSYSGLFDATQTKW 300

Qy 301 EVDGSOLVKVVSWYDNEMSYTAQLYRTLEYFAKIAK 336
 Db 301 TVDGNQLVKVVSWYDNEMSYTSQVLRTLEYFAKIAK 336

RESULT 13

AAM50640
 ID AAM50640 standard; protein; 336 AA.
 AC AAM50640;
 XX DT 04-APR-2002 (first entry)

XX (UYSA-) UNIV SASKATCHEWAN.
 XX KW antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
 XX gene therapy; vaccine.
 PI XX Streptococcus pneumoniae; type 4 strain.
 XX WPI: 2002-AJ, Perez-Casal J, Fontaine M, Potter AA;
 XX DR 2002-130725/17.
 XX DR N-PSDB; ABA91249.
 XX PT Novel isolated GapC protein of Streptococcus dysgalactiae, *S. agalactiae*,
 PT *S. suis*, *S. parauensis*, or *S. iniae*, useful as vaccine component for
 PT treating streptococcal infection which causes mastitis in vertebrates.
 PS XX S. agalactiae, *S. suis*, *S. parauensis*, or *S. iniae*, useful as vaccine component for
 PS treating streptococcal infection which causes mastitis in vertebrates.
 PS XX PS (CHIR.) CHIRON SPA,
 CC PA (GENC-) INST GENOMIC RES
 CC PA XX PI Masiognani V, Tettelin H, Fraser C;
 CC PR XX DR WPI: 2003-040579/03.
 CC PR XX DR N-PSDB; ABX07806.
 CC PT New proteins and nucleic acid molecules from *Streptococcus pneumoniae*,
 CC PT useful as medicaments for treating or preventing a disease or infection
 CC PT due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
 CC PT ear infection.
 CC XX Claim 1; SEQ ID NO 4188; 562P; English.
 CC XX The invention relates to a protein comprising or having at least 50%
 CC identity to any of the 2469 amino acid sequences, identified in the
 CC specification (available on a computer readable format), or its fragment,
 CC expressed from 2469 of 2489 identical DNA coding regions from the
 CC *Streptococcus pneumoniae* type 4 strain genomic sequence appearing as
 CC AB5654. Also included are an antibody which binds one of the proteins,
 CC treating a patient by administering the protein, DNA or antibody (in a
 CC composition), a kit comprising first and second primers, which are the
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a
 CC sequence not defined in the specification, for amplifying a target
 CC sequence contained within a *Streptococcus* nucleic acid sequence, where
 CC the first primer is substantially complementary to the target sequence
 CC and the second primer is substantially complementary to the complement of
 CC the target sequence, and where the pairs of the primers having
 CC substantially complementary define the termini of the target sequence to
 CC be amplified, assay comprising contacting a test compound with the
 CC protein, and determining whether the test compound binds to the protein
 CC and a *Streptococcus pneumoniae* bacterium, where one or more genes
 CC encoding the proteins, nucleic acid molecules, antibody and compositions are useful
 CC for treating or preventing a disease or infection due to *streptococcus*
 CC bacteria, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis
 CC media or ear infection. They are also useful in developing vaccines,
 CC diagnostics and antibiotics. The methods are useful for identifying
 CC immunodominant proteins. The present sequence is one of the 2469 proteins
 CC expressed by the identified coding regions from the genomic sequence.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences). (Updated on 23-Oct-2003 to
 CC standardise OS field)
 XX SQ Sequence 335 AA;
 Query Match 93.4%; Score 1602; DB 5; Length 336;
 Best Local Similarity 91.7%; Pred. No 1, 1.e-134;
 Matches 300; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 M V V K V G I N G P R I G R I G L A F R R I Q N V G E V T R I N D L D P M M L A H I L K Y D T T Q G F D G T V E Y 60
 Db 1 M V V K V G I N G P R I G R I G L A F R R I Q N V G E V T R I N D L D P M M L A H I L K Y D T T Q G F D G T V E Y 60
 Qy 121 T A P G N D V T V V F V T N H D I L D G T E V I S A S C T N C L P M A K A L H D A F G I Q K G L M T I H A 180
 Db 121 T A P G N D V T V V F V T N H D I L D G T E V I S A S C T N C L P M A K A L H D A F G I Q K G L M T I H A 180
 Qy 61 K E G G P E V N G P I K V S A E R D P E N I D M A T D P V E I V L E A T G F P K K E A K E C H L H A N G A K V V 120
 Db 61 K E G G P E V N G P I K V S A E R D P E N I D M A T D P V E I V L E A T G F P K K E A K E C H L H A N G A K V V 120
 Qy 181 Y T G D M I L D P H R G G D L R A R A G A N I V N S T G A K A I G L V I B L N G K L D G A Q R V P V T 240
 Db 181 Y T G D M I L D P H R G G D L R A R A G A N I V N S T G A K A I G L V I B L N G K L D G A Q R V P V T 240
 Qy 241 G S V T E L V V T L D K N V S D E I N A A M K A A S D F G T Y T D P V S S D I V G V S Y G S L F D A T Q T K V M 300
 Db 241 G S V T E L V V T L D K N V S D E I N A A M K A A A N T S Y G T D P V S S D I V G I S S G S L F D A T Q T K V M 300
 Qy 301 E V D G S Q L V K V Y S W D N E M S Y T A Q L Y R T E Y F A K I A K 336
 Db 301 T V D G N Q L V K V Y S W D N E M S Y T A Q L Y R T E Y F A K I A K 336
 SQ Sequence 335 AA;
 Query Match 92.9%; Score 1593.5; DB 6; Length 335;
 Best Local Similarity 92.6%; Pred. No. 6.3e-134;
 Matches 311; Conservative 12; Mismatches 12; Indels 1; Gaps 1;
 AC 1 M V V K V G I N G P R I G R I G L A F R R I Q N V G E V T R I N D L D P M M L A H I L K Y D T T Q G F D G T V E Y 60
 AC 1 M V V K V G I N G P R I G R I G L A F R R I Q N V G E V T R I N D L D P M M L A H I L K Y D T T Q G F D G T V E Y 60
 DT 61 K E G G P E V N G P I K V S A E R D P E N I D M A T D P V E I V L E A T G F P K K E A K E C H L H A N G A K V V 120
 DT 61 K E G G P E V N G P I K V S A E R D P E Q I D M A T D G V E I V L E A T G F P K K E A K E C H L H A N G A K V V 119
 S. pneumoniae type 4 strain protein from coding region #2094.
 DB S. pneumoniae; pneumonia; sepsis; otitis media; ear infection;
 XX Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;

Qy 121 TAPGGNDVKTIVFNTNHDILDGTEVIGASCTTNCALPMAKALHDAGIQKGMLTTIHA 180
 Db 120 TAPGGNDVKTIVFNTNHDILDGTEVIGASCTTNCALPMAKALQDNFVVEGMLTTIHA 179
 Qy 181 YTGQMDMILDGPARGGDLRARAAGANTVPNSTGAAKAIGLVPEUNGKLDGAQRPVPT 240
 Db 180 YTGQMDMILDGPARGGDLRARAAGANTVPNSTGAAKAIGLVPEUNGKLDGSAQRVPT 239
 Qy 241 GSYTELTVLTDKQVSYDVEINAMKASNSDFTGTYEDPIVSSDIVGVSYGSLSFDATQTKM 300
 Db 240 GSYTELIVLAVLEKRVTDVEINAMKASNSDFTGTYEDPIVSSDIVGMSYGSLSFDATQTKL 299
 Qy 301 EVDGSOLVAKVSYWDNEMSYTAQLVRLTEYFAKIAK 336
 Db 300 DVGKQLRKVSYWDNEMSYTAQLVRLTEYFAKIAK 335

RESULT 15
 AAU37576 ID AAU37576 standard; protein; 359 AA.
 XX AC AAU37576;
 XX DT 14-FEB-2002 (first entry)
 XX DE Streptococcus pneumoniae cellular proliferation protein #5.
 XX KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 XX antibacterial; drug design.
 XX OS Streptococcus pneumoniae.
 XX WO200170955-A2.
 XX PN 27-SEP-2001.
 XX PR 21-MAR-2001; 2001WO-US009180.
 XX PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207722P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253623P.
 PR 22-DEC-2000; 2000US-0257933P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX PA (ELITR) - ELITRA PHARM INC.
 XX PI Haselbeck R, Ohlsen KB, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX DR; 2001-611495/70.
 XX N-PSDB; AAS55435.

PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX Example 3; SEQ ID NO 13169; 511PP; English.

XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, *Staphylococcus aureus* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic

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Omni.protein - protein search, using sw model1

Run on: May 11, 2004, 16:46:47 ; Search time 23 Seconds (without alignment)

754.188 Million cell updates/sec

Title: US-10-650-369-12

Perfect score: 1715

Sequence: 1 MVKVGINGFGRIGLAFRR.....EMSYTAQLVRLTVEFAKIAK 336

Scoring table: BL0SUM62

GapOp 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents (AA-*)

1: /cn2-6/ptodata/2/iaa/SA-COMB.pep:*

2: /cn2-6/ptodata/2/iaa/5B-COMB.pep:*

3: /cn2-6/ptodata/2/iaa/SA-COMB.pep:*

4: /cn2-6/ptodata/2/iaa/6B-COMB.pep:*

5: /cn2-6/ptodata/2/iaa/PCUTS-COMB.COMB.pep:*

6: /cn2-6/ptodata/2/iaa/BackTitles1.pep:*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match length DB ID

Result No.	Score	Match length	DB ID	Description
1	1715	100.0	336 4 US-09-878-766A-12	Sequence 12, Appl
2	1711	99.8	336 1 US-07-928-462-2	Sequence 2, Appl
3	1711	99.8	336 3 US-08-273-247-2	Sequence 2, Appl
4	1656.5	96.6	448 4 US-03-878-766A-12	Sequence 16, Appl
5	1618.5	94.3	336 4 US-03-878-766A-16	Sequence 14, Appl
6	1602	93.4	336 4 US-03-878-766A-14	Sequence 20, Appl
7	1584	92.4	336 4 US-03-878-766A-20	Sequence 18, Appl
8	1578	92.4	336 4 US-03-878-766A-18	Sequence 54, Appl
9	1549.5	90.3	333 3 US-08-961-083-44	Sequence 54, Appl
10	1549.5	90.3	333 4 US-09-536-784-54	Sequence 4400, AP
11	1337.5	78.0	346 4 US-03-134-000C-4400	Sequence 4769, AP
12	1325.5	77.3	333 4 US-09-107-532A-4769	Sequence 5513, AP
13	1190	69.4	348 4 US-09-134-001C-5513	Sequence 4229, AP
14	967	56.4	357 4 US-03-134-000C-4229	Sequence 233, APP
15	956	56.3	349 4 US-09-489-039A-13939	Sequence 13939, AP
16	959	55.9	349 4 US-09-489-039A-13939	Patent No. 5290610
17	896.5	52.3	335 6 5290590-9	Patent No. 5290610
18	885.5	51.6	334 6 5290590-10	Sequence 7679, AP
19	835.5	48.7	334 6 5290590-11	Sequence 205, APP
20	830	48.4	325 4 US-03-489-039A-7679	Sequence 205, APP
21	824.5	48.1	340 3 US-03-095-855-105	Sequence 205, APP
22	824.5	48.1	340 4 US-09-205-426-205	Sequence 8083, AP
23	799	46.6	340 4 US-09-543-681A-8083	Sequence 9410, AP
24	770.5	44.9	352 4 US-03-489-039A-9410	Sequence 4057, AP
25	766.5	44.7	282 4 US-09-107-532A-4057	Sequence 662, APP
26	740.5	43.2	336 4 US-09-198-452A-662	Sequence 10, APP
27	736	42.9	338 4 US-03-091-725-10	Sequence 19846, A

ALIGNMENTS

RESULT 1
US-09-878-766A-12

/ Sequence 12, Application US/09878766A

/ Patent No. 6602700

/ GENERAL INFORMATION:

/ APPLICANT: Pottier, Andrew A.

/ ATTORNEY: Perec-Casal, Jose

/ TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN

/ TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION

/ FILE REFERENCE: 900-0057

/ CURRENT APPLICATION NUMBER: US/09-878B, 766A

/ CURRENT FILING DATE: 2001-09-10

/ NUMBER OF SEQ ID NOS: 22

/ SOFTWARE: Patentin Ver. 2.0

/ SEQ ID NO: 12

/ LENGTH: 336

/ TYPE: PRT

/ ORGANISM: Streptococcus dysgalactiae

US-09-878-766A-12

Query Match 100 0%; Score 1715; DB 4; Length 336;

Best Local Similarity 100 0%; Pred. No. 4.2e-164;

Matches 336; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVKVINGFGRIGLAFRIQVNGEGVTRINDLTDPMNLHLKLYKDITQGREGCTVEV 60

Db 1 MVVKVINGFGRIGLAFRIQVNGEGVTRINDLTDPMNLHLKLYKDITQGREGCTVEV 60

Qy 61 KEGGPPVNGFNIKSAERDENTIDATGVEIVLEATGFPAKKAEEKLHANGAKVVI 120

Db 61 KEGGPPVNGFNIKSAERDENTIDATGVEIVLEATGFPAKKAEEKLHANGAKVVI 120

Qy 121 TAPGNDVXPTVNTNDLDGTETVVISGASCTINCLAPMAKALDAFGTQKGMLMTIHA 180

Db 121 TAPGNDVXPTVNTNDLDGTETVVISGASCTINCLAPMAKALDAFGTQKGMLMTIHA 180

Qy 181 YTGDQMLDGFHGRGDLRRAAGANTIVNSTGAKAIGVPELNKGKLGAAQRPVPT 240

Db 181 YTGDQMLDGFHGRGDLRRAAGANTIVNSTGAKAIGVPELNKGKLGAAQRPVPT 240

Qy 241 GSVTELVVTLDKSYDEINAAMKAANSFGTGTEDPTVSDIVGVSGLFDATQTKW 300

Db 241 GSVTELVVTLDKSYDEINAAMKAANSFGTGTEDPTVSDIVGVSGLFDATQTKW 300

RESULT 2
US-07-928-462-2
Sequence 2, Application US/07928462

Patent No. 538996

GENERAL INFORMATION:

APPLICANT: Boyle, Michael D.P.

APPLICANT: Broder, Christopher C.

APPLICANT: von Mering, Gregory O.

TITLE OF INVENTION: Bacterial Plasmin Receptors as

TITLE OF INVENTION: Bacterial Plasmin Receptors as

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/928,462

FILING DATE: 1992/08/10

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/524,411

FILING DATE: 16-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/330,849

FILING DATE: 29-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UF/S&S-13.C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 336 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;
Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;
Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

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Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Query Match Score 99.8%; Score 1711; DB 1; Length 336;

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US-07-928-462-2

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

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US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

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US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

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US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

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US-07-928-462-2

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

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US-07-928-462-2

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Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

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Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

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Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

US-07-928-462-2

Query Match Score 99.8%; Score 1711; DB 1; Length 336;

Best Local Similarity 99.4%; Pred. No. 1.e-163; DB 3;

RESULT 4

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Db 241 GSYTELVYTLDKVNSVDEINAMKAASNDSFQTYTEDPIVSSDIVGVSQGLFDATOTKYM 300

Qy 301 EVDGSQLVTKVSYWDNEASYTQLVRLTEYFAKIAK 336
Db 301 EVDGSQLVTKVSYWDNEASYTQLVRLTEYFAKIAK 336

Query Match 96.6%; Score 1656.5; DB 4; Length 448;
Best Local Similarity 79.6%; Pred. No. 5.1e-158; Indels 85; Gaps 1;

Matches 335; Conservative 0; Mismatches 1;

Qy 1 MVVKVINGFGRIGLAFRIONVEVTRINDLDPNMLAHLKYDTQGRFDGTVY 60
Db 28 MVVKVINGFGRIGLAFRIONVEVTRINDLDPNMLAHLKYDTQGRFDGTVY 87

Qy 61 KEGGFVYNGNFVTKYSAEDPENIDWATGTVYVLEATGFFAKKEAEKHLHANGAKVYI 120
Db 61 KDGAFEVNNGNFVTKYSAEDPENIDWATGTVYVLEATGFFAKKEAEKHLHANGAKVYI 120

Qy 121 TAPGSDNDVTKVVENTNHDILDGTETVVISGASCTNCLAPMAKALHDAGIQKGLMTTHA 180
Db 121 TAPGSDNDVTKVVENTNHDILDGTETVVISGASCTNCLAPMAKALQDNFGVKQGLMTTHA 180

Qy 181 YTGDQMTLJDGPHRGDDLRARRAGANIVPNSTGRAKAIGLVLPELNGKLDAQQRVPVPT 240
Db 181 YTGDQMTLJDGPHRGDDLRARRAGASNIIPNSTGAAIGLVLPELNGKLDAQQRVPVPT 240

Qy 241 GSVDTELVYTLDKVNSVDEINAMKAASNDSFQTYTEDPIVSSDIVGVSQGLFDATOTKYM 300
Db 241 GSVDTELVYTLDKVNSVDEINAMKAASNDSFQTYTEDPIVSSDIVGVSQGLFDATOTKYM 300

Qy 301 EVDGSQLYRKVSYWDNEASYTAOLVRLTEYFAKIAK 336
Db 301 TVDENQLYRKVSYWDNEASYTAOLVRLTEYFAKIAK 336

RESULT 6

Qy 148 KDFEQIDWATDGVEIVLIDGTIVEVKEGGFENQFQVKVAAEREPAVIDATDGVEIVL 207
Qy 96 ATSFPAKKEAEKHLHANGAKVYITAGVNTVPAQRLVRLTEYFAKIAK 155
Db 208 ATSFPAKKEAEKHLHANGAKVYITAGVNTVPAQRLVRLTEYFAKIAK 267

Qy 156 CLAPMAKALHDAGIQKGLMTTHATGQMDLQJDGPHRGDDLRARRAGANIVPNSTGAA 215
Db 268 CLAPMAKALHDAGIQKGLMTTHATGQMDLQJDGPHRGDDLRARRAGANIVPNSTGAA 327

Qy 216 KAIGLVLPELNGKLDAQRPVPTGSVTELYVTLDKVNSVDEINAMKAASNDSFQTYE 275
Db 326 KAIGLVLPELNGKLDAQRPVPTGSVTELYVTLDKVNSVDEINAMKAASNDSFQTYE 387

Qy 276 DPIVSSDIVGVSQGLFDATOTKYMEDGSQLVTKVSYWDNEASYTAOLVRLTEYFAKIA 335
Db 388 DPIVSSDIVGVSQGLFDATOTKYMEDGSQLVTKVSYWDNEASYTAOLVRLTEYFAKIA 447

Qy 336 K 336
Db 448 K 448

Query Match 93.4%; Score 1602; DB 4; Length 336;
Best Local Similarity 91.7%; Pred. No. 9.9e-153; Indels 0; Gaps 0;

Matches 308; Conservative 17; Mismatches 11;

RESULT 5

Qy 1 Sequence 16, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0057
; CURRENT APPLICATION NUMBER: US/09/878,766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 16
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus uberis
US-09-878-766A-16

Query Match 94.3%; Score 1618; DB 4; Length 336;
Best Local Similarity 92.9%; Pred. No. 2.4e-154;
Matches 312; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MVVKVINGFGRIGLAFRIONVEVTRINDLDPNMLAHLKYDTQGRFDGTVY 60
Db 1 MVVKVINGFGRIGLAFRIONVEVTRINDLDPNMLAHLKYDTQGRFDGTVY 60

Qy 61 KEGGFVYNGNFVTKYSAEDPENIDWATGTVYVLEATGFFAKKEAEKHLHANGAKVYI 120
Db 61 KDGAFEVNNGNFVTKYSAEDPENIDWATGTVYVLEATGFFAKKEAEKHLHANGAKVYI 120

Qy 121 TAPGSDNDVTKVVENTNHDILDGTETVVISGASCTNCLAPMAKALHDAGIQKGLMTTHA 180
Db 121 TAPGSDNDVTKVVENTNHDILDGTETVVISGASCTNCLAPMAKALQDNFGVKQGLMTTHA 180

Qy 181 YTGDQMTLJDGPHRGDDLRARRAGANIVPNSTGRAKAIGLVLPELNGKLDAQQRVPVPT 240
Db 181 YTGDQMTLJDGPHRGDDLRARRAGASNIIPNSTGAAIGLVLPELNGKLDAQQRVPVPT 240

Qy 241 GSVDTELVYTLDKVNSVDEINAMKAASNDSFQTYTEDPIVSSDIVGVSQGLFDATOTKYM 300
Db 241 GSVDTELVYTLDKVNSVDEINAMKAASNDSFQTYTEDPIVSSDIVGVSQGLFDATOTKYM 300

Qy 301 EVDGSQLYRKVSYWDNEASYTAOLVRLTEYFAKIAK 336
Db 301 TVDENQLYRKVSYWDNEASYTAOLVRLTEYFAKIAK 336

Qy 1 Sequence 14, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
; FILE REFERENCE: 9000-0057
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 14
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-09-878-766A-14

Query Match 93.4%; Score 1602; DB 4; Length 336;
Best Local Similarity 91.7%; Pred. No. 9.9e-153; Indels 0; Gaps 0;

Matches 308; Conservative 17; Mismatches 11;

US-09-09-878-766A-16

RESULT 8
US-09-878-766A-18
; Sequence 18, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; FILE REFERENCE: 900-0057
; CURRENT APPLICATION NUMBER: US/09/878, 766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 18
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus parauberis
; US-09-878-766A-18

Query 1 MVVKVINGFGRGLAFRIQVTRINDLTDPMMLAHILKDTTQGRFDGIVEV 60
Database 1 MVVKVINGFGRGLAFRIQVTRINDLTDPMMLAHILKDTTQGRFDGIVEV 60
Query 1 KEGGFVNQFNFYKVAERPDNITDGTIVLEATGFFAKKEAEEGHILHANGAKVYI 120
Database 1 KEGGFVNQFNFYKVAERPDNITDGTIVLEATGFFAKKEAEEGHILHANGAKVYI 120
Query 121 TAPGNDVKTIVFNTNHDILDGTETVSGASCTINCLAMAKALDAFGIQLGMLTTHA 180
Database 121 TAPGNDVKTIVFNTNHDILDGTETVSGASCTINCLAMAKALDAFGIQLGMLTTHA 180
Query 181 YTGDQMLDGPGRGSDLRARAAGAANIVPNSTGAAKAGLVIPELNGKLDGAQRVPVPT 240
Database 181 YTGDQMLDGPGRGSDLRARAAGAANIVPNSTGAAKAGLVIPELNGKLDGAQRVPVPT 240
Query 241 GSVTLLVYTLDKNTVSYDTEINAMKAASNDSEGTIDPIVSSDIVGVSYGSLEPATOKVY 300
Database 241 GSVTLLVYTLDKNTVSYDTEINAMKAASNDSEGTIDPIVSSDIVGVSYGSLEPATOKVY 300
Query 301 EVDGSOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336
Database 301 EVDGSOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336
Query 301 TVDGNOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336
Database 301 TVDGNOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336

RESULT 7
US-09-878-766A-20
; Sequence 20, Application US/09878766A
; Patent No. 6660270
; GENERAL INFORMATION:
; APPLICANT: Potter, Andrew A.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; FILE REFERENCE: 900-0057
; CURRENT APPLICATION NUMBER: US/09/878, 766A
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 20
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus iniae
; US-09-878-766A-20

Query 1 MVVKVINGFGRGLAFRIQVTRINDLTDPMMLAHILKDTTQGRFDGIVEV 60
Database 1 MVVKVINGFGRGLAFRIQVTRINDLTDPMMLAHILKDTTQGRFDGIVEV 60
Query 1 KEGGFVNQFNFYKVAERPDNITDGTIVLEATGFFAKKEAEEGHILHANGAKVYI 120
Database 1 KEGGFVNQFNFYKVAERPDNITDGTIVLEATGFFAKKEAEEGHILHANGAKVYI 120
Query 121 TAPGNDVKTIVFNTNHDILDGTETVSGASCTINCLAMAKALDAFGIQLGMLTTHA 180
Database 121 TAPGNDVKTIVFNTNHDILDGTETVSGASCTINCLAMAKALDAFGIQLGMLTTHA 180
Query 181 YTGDQMLDGPGRGSDLRARAAGAANIVPNSTGAAKAGLVIPELNGKLDGAQRVPVPT 240
Database 181 YTGDQMLDGPGRGSDLRARAAGAANIVPNSTGAAKAGLVIPELNGKLDGAQRVPVPT 240
Query 241 GSVTLLVYTLDKNTVSYDTEINAMKAASNDSEGTIDPIVSSDIVGVSYGSLEPATOKVY 300
Database 241 GSVTLLVYTLDKNTVSYDTEINAMKAASNDSEGTIDPIVSSDIVGVSYGSLEPATOKVY 300
Query 301 EVDGSOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336
Database 301 EVDGSOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336

RESULT 9
US-08-961-083-54
; Sequence 54, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP CODE: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 466/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:

Query 1 KEGGFVNQFNFYKVAERPDNITDGTIVLEATGFFAKKEAEEGHILHANGAKVYI 120
Database 1 KEGGFVNQFNFYKVAERPDNITDGTIVLEATGFFAKKEAEEGHILHANGAKVYI 120
Query 121 TAPGNDVKTIVFNTNHDILDGTETVSGASCTINCLAMAKALDAFGIQLGMLTTHA 180
Database 121 TAPGNDVKTIVFNTNHDILDGTETVSGASCTINCLAMAKALDAFGIQLGMLTTHA 180
Query 181 YTGDQMLDGPGRGSDLRARAAGAANIVPNSTGAAKAGLVIPELNGKLDGAQRVPVPT 240
Database 181 YTGDQMLDGPGRGSDLRARAAGAANIVPNSTGAAKAGLVIPELNGKLDGAQRVPVPT 240
Query 241 GSVTLLVYTLDKNTVSYDTEINAMKAASNDSEGTIDPIVSSDIVGVSYGSLEPATOKVY 300
Database 241 GSVTLLVYTLDKNTVSYDTEINAMKAASNDSEGTIDPIVSSDIVGVSYGSLEPATOKVY 300
Query 301 EVDGSOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336
Database 301 EVDGSOLVKVSVWYDNEMSYTAQLVRLTEYFAKAK 336

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APPLICATION NUMBER: US/08/9961,083
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPLOGY: linear
MOLECULE TYPE: protein
US-08-991-083-54

Query Match 90.3% Score 15
Best Local Similarity 91.3% Pred. No.
Matches 303; Conservative 12; Misra

Qy      2 VVKVINGFGRIGRLAARRIONVQEYEV
Db      1 VVKVINGFGRIGRLAARRIONVQEYEV

Qy      62 EGGEGEVNGFPIKVSAAERPDENDWATDG
Db      61 EGGEVNGFPIKVSAAERPDENDWATDG

Qy      122 APGENDVTKVVFNTNHDLDGTETVISG
Db      120 APGENDVTKVVFNTNHDLDGTETVISG

Qy      182 TGDMDMILGPHRGDGLRARGANITV
Db      180 TGDMDMILGPHRGDGLRARGANITV

Qy      242 SVEILVILTDKNTSYDEINANKAASND
Db      240 SVEILVATEKNTYDTEINANKAASNE

Qy      302 VDGSQLVVKVSWYDNEMSYAQLVRLTLE
Db      300 VDGSQLVVKVSWYDNEMSYAQLVRLTLE

RESULT 10
US-09-536-784-54
; Sequence 54, Application US/09536784
; Patent No. 6570082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus
; NUMBER OF SEQUENCES: 432
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Science
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5"
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS ver.
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/53

```

RESULT 11
US-09-134-000C-4400
Sequence 4400 Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynd Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134.000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4400
LENGTH: 346
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-4400
Query Match 78.0% Score 1337.5; DB 4; Length 346;

RESULT 10
US-09-536-784-54
Sequence 54 Application US/09536784
Patent No. 6573082

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: *Streptococcus pneumoniae Antigens and Vaccines*
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra, HP 486/33
OPERATING SYSTEM: MS/DOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536-784
Query No. US-09-134

Best Local Similarity 78.4%; Pred. No. 4.1e-126; Indels 1; Gaps 1;
 Matches 262; Conservative 24; Mismatches 1; Location: (B) LOCATION 1.; SEQ ID NO: 4769;

Qy 1 MVRVQINGFGRIGLARRRIVRINDIDPNMLAHLLKIDTQGRDGTVY 60
 Db 14 MTKVQINGFGRIGLARRRIVRINDIDPNMLAHLLKIDTQGRFQTVY 73
 Qy 61 KEGGFYNGNFTIKSAERDPENIDATGVBIVLBEATGFFAKKBAEKLHANGAKVYI 120
 Db 74 HEGSFNQGKELKVLNRPFLPELPGELDIVECTGFTSKAEEKLLTA-GAKVYI 132
 Qy 121 TAPGNDVKTQVTFNTNHDILDGTETVIGSASCTINCLPMAKALHDAFGIQKGLMTIHA 180
 Db 133 SAPPGNDVPTVYNTNHTLTGEETVIGSASCTINCLPMAKALHDAFGIQKGLMTIHA 192
 Qy 181 YTGDNMTLDPHRRGDLRARAAGANIVPSTGAKAIGLIVIPELNGKDLGAQRPVYET 240
 Db 193 YTGDNMTLDPHRRGDLRARAAGANIVPSTGAKAIGLIVIPELNGKDLGAQRPVYAT 252
 Qy 241 GSVTELYVTDKNSVDEINAKMAKSNDSGFTEDPVISSDIVGVSQYSSLFQDATQTKW 300
 Db 253 GSILTELYVTDKNSVDEINAKMAKSNDSGFTEDPVISSDIVGVSQYSSLFQDATQTKW 312
 Qy 301 EVDGSQLVKVSQWYDNEMSYTAQLYRTLEYPAKI 334
 Db 313 TVGDQKLVKTVAYWDNEMSYTAQLYRTLEYFANL 346

RESULT 13
 US-09-134-001C-5513
 / Sequence 4769, Application US/09107532A
 / Patent No. 658,275
 / GENERAL INFORMATION:
 / APPLICANT: Lynn A. Doucette-Stamm and David Bush,
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 / ENTEROCOCCUS FAEBUM FOR DIAGNOSTICS AND THERAPEUTICS
 / NUMBER OF SEQUENCES: 73:10
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 / STREET: 100 Beaver Street
 / CITY: Waltham
 / STATE: Massachusetts
 / COUNTRY: USA
 / ZIP: 024354
 / COMPUTER READABLE FORM: CD/ROM ISO9660
 / MEDIUM TYPE: PC
 / COMPUTER: PC
 / OPERATING SYSTEM: <Unknown>
 / SOFTWARE: ASCII
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/107,532A
 / FILING DATE: 30-Jun-1998
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 60/085,598
 / FILING DATE: 14 May 1998
 / APPLICATION NUMBER: 60/051571
 / FILING DATE: July 2, 1997
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Arinieillo, Pamela, Denice
 / REGISTRATION NUMBER: 40,489
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (781)993-5007
 / TELEFAX: (781)993-8277
 / INFORMATION FOR SEQ ID NO: 4769:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 333 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: YES
 / ORIGINAL SOURCE: ORGANISM: Enterococcus faecium

FEATURE: NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1.; SEQ ID NO: 4769;
 / Query Match 77.3%; Score 1325.5; DB 4; Length 333;
 / Best Local Similarity 77.8%; Pred. No. 6.3e-125;
 / Mismatches 25; Conservative 48; Indels 1; Gaps 1;
 / Matches 260;
 Qy 1 MTKVQINGFGRIGLARRRIVRINDIDPNMLAHLLKIDTQGRFQTVY 60
 Db 1 MTKVQINGFGRIGLARRRIVRINDIDPNMLAHLLKIDTQGRFQTVY 60
 Qy 61 KEGGFYNGNFTIKSAERDPENIDATGVBIVLBEATGFFAKKBAEKLHANGAKVYI 120
 Db 61 HEGSFNQGKELKVLNRPFLPELPGELDIVECTGFTSKAEEKLLTA-GAKVYI 119
 Qy 121 TAPGNDVKTQVTFNTNHDILDGTETVIGSASCTINCLPMAKALHDAFGIQKGLMTIHA 180
 Db 120 SAPPGNDVPTVYNTNHTLTGKETVIGSASCTINCLPMAKALHDAFGIQKGLMTIHA 179
 Qy 181 YTGDNMTLDPHRRGDLRARAAGANIVPSTGAKAIGLIVIPELNGKDLGAQRPVYET 240
 Db 180 YTGDNMTLDPHRRGDLRARAAGANIVPSTGAKAIGLIVIPELNGKDLGAQRPVYAT 252
 Qy 241 GSVTELYVTDKNSVDEINAKMAKSNDSGFTEDPVISSDIVGVSQYSSLFQDATQTKW 300
 Db 240 GSILTELYVTDKNSVDEINAKMAKSNDSGFTEDPVISSDIVGVSQYSSLFQDATQTKW 312
 Qy 301 EVDGSQLVKVSQWYDNEMSYTAQLYRTLEYPAKI 334
 Db 300 TVGDQKLVKTVAYWDNEMSYTAQLYRTLEYFANL 346

RESULT 13
 US-09-134-001C-5513
 / Sequence 5513, Application US/09134001C
 / Patent No. 638,370
 / GENERAL INFORMATION:
 / APPLICANT: Lynn Doucette-Stamm et al.
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 / FILE REFERENCE: GTC-007
 / CURRENT APPLICATION NUMBER: US/09/134,001C
 / PRIOR APPLICATION NUMBER: US 60/064,964
 / CURRENT FILING DATE: 1998-08-13
 / PRIOR FILING DATE: 1997-11-08
 / PRIOR APPLICATION NUMBER: US 60/055,779
 / PRIOR FILING DATE: 1997-08-14
 / NUMBER OF SEQ ID NOS: 5674
 / SEQ ID NO: 5513
 / LENGTH: 348
 / TYPE: PRT
 / ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-5513
 / Query Match 69.4%; Score 1190; DB 4; Length 348;
 / Best Local Similarity 69.4%; Pred. No. 2.9e-111;
 / Mismatches 234; Conservative 39; Indels 2; Gaps 2;
 / Matches 234;
 Qy 1 MTKVQINGFGRIGLARRRIVRINDIDPNMLAHLLKIDTQGRFQTVY 60
 Db 13 MTKVQINGFGRIGLARRRIVRINDIDPNMLAHLLKIDTQGRFQTVY 72
 Qy 61 KEGGFYNGNFTIKSAERDPENIDATGVBIVLBEATGFFAKKBAEKLHANGAKVYI 120
 Db 73 IEFGFQYNGKELKVLNRPFLPELPGELDIVECTGFTSKAEEKLLTA-GAKVYI 131
 Qy 121 TAPGNDVKTQVTFNTNHDILDGTETVIGSASCTINCLPMAKALHDAFGIQKGLMTIHA 180
 Db 122 SAPGKDVKTIVTFNTNHDILDGTETVIGSASCTINCLPMAKALHDAFGIQKGLMTIHA 191

RESULT 14

US-10-650-369-12.rai

Sequence 4229, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032296-032

CURRENT APPLICATION NUMBER: US 09/134, 000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055, 778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 4229

LENGTH: 357

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-4229

Query Match 56.4%; Score 967; DB 4; Length 357;

Best Local Similarity 58.3%; Pred. No. 8e-89; Mismatches 91; Indels 6; Gaps 5;

Matches 199; Conservative 44; Mismatches 91; Indels 6; Gaps 5;

Qy 1 MVKVKGNGFGRIGLAFRRQIINY-EGVEVTRINDLTDPMNLALHLKYYDTTGRFDGTV 59

Db 22 MTKVKGNGFGRIGLAFRRQIINY-EGVEVTRINDLTDPMNLALHLKYYDTTGRFDGTV 81

Qy 60 VKEGGFPEVGNFIKVAERDPENIDWATP-GVEVLEATGFFAKKEAERKHLHANGAKKV 118

Db 82 ATENGGVNDDEETVVAEEDASKP1PKWVQD1VLECTGFTSE3EAQAHIDA-GVTKRV 140

Qy 119 VITARGGNDKVKTKVNTNHDLDSTETVVAEEDASKP1PKWVQD1VLECTGFTSE3EAQAHIDA-GVTKRV 178

Db 141 VISAAG-AMKTTIVNNDLTDANDK1SAGSCTTCA1PMAK1HDA-GVTKRV 199

Qy 179 HAYTQDMMLDGPGRGDD1RARRGAANIVPNSTGAAG1GLV1PELNGKLQGAQ3PV 238

Db 200 HAYTQDMMLDGPGRGDD1RARRGAANIVPNSTGAAG1GLV1PELNGKLQGAQ3PV 259

Qy 239 PTGSVTEVNLTKRVS1BNAAMK--AASNDSFGYTEDPIVSSDIVGVSYGSLSLPATQ 296

Db 260 VDGSLTE1L1SLKTKVTAQVNNEAMKHTIDNSFGYDREIVSGD1IGTBSG1FDPQ 319

Qy 297 TKYMEVDGGSOLVKVSYWDNEMSYTAQOLVRLTEYFAK1 334

Db 320 TEVTAGDQFLQVKTVW1DNEYGFTCQMTLLEKFanL 357

RESULT 14

US-09-634-238-233

Query Match 56.3%; Score 966; DB 4; Length 340;

Best Local Similarity 57.0%; Pred. No. 9.4e-89; Mismatches 89; Indels 10; Gaps 6;

Matches 195; Conservative 48; Mismatches 89; Indels 8; Gaps 6;

Qy 1 MVVKVKGNGFGRIGLAFRRQIINY---EVEVEVTRINDLTDPMNLALHLKYYDTTGRFDG 56

Db 1 MTKVKGNGFGRIGLAFRRQIINY-EVAKSNDIQQVAVNDLTSPTMLALHLKYYDTTGRFDG 60

Qy 57 TVEVKEGGFPEVGNFIKVAERDPENIDWATDGVETVLEATGFFAKKEAERKHLHANGA 115

Db 61 EVSATANGIVVDGKGYRVTAAEPQAGNIPMVKNDGVDVLCCTGFTSAEKSQAHDA-GA 119

Qy 116 KKVVV-TAPGENDVKTVENTNHDLDGTETVSGASCTTCLAPMAKALHDAGFCTQGLM 175

Db 120 KRVLISAPACK-IKTVVNTYNNDDTNAADDK1SAGSCTTCLAPMAF1NQERGLIEVGTM 178

Qy 176 TTIHAYTQDMMLDGPGRGDD1RARRGAANIVPNSTGAAG1GLV1PELNGKLQGAQ 235

Db 179 TTIVHAYTQSTOML1DGPVRGNNLRAA-SAAANTIPHS1TGAAG1GLV1PELNGKLQGAQ 238

Qy 236 VPVPTGSVTEVNLTKRVS1BNAAMK--AASNDSFGYTEDPIVSSDIVGVSYGSLSF 292

Db 239 VSVVBDSLTLVSLKTKVTAQVNNEAMKHTIDNSFGYDREIVSGD1IGTBSG1FDPQ 298

Qy 293 DATOTKVMEDGGSOLVKVSYWDNEMSYTAQOLVRLTEYFAK1 334

Db 299 DPTQTVTTAGDQ1VTKTVAWYDNEYGFTCQMTLLEKFanL 340

Search completed: May 11, 2004, 16:50:40

Job time : 42 secs

RESULT 15

US-09-634-238-233

Sequence 233, Application US/09634233

Patent No. 6544772

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Havukkala, Ilkka J.

APPLICANT: Bloksberg, Leonard, N.

APPLICANT: Lubbers, Mark W.

APPLICANT: Dekker, James

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OM protein - protein search, using sw model

Run on: May 11, 2004, 16:45:46 ; Search time 21 Seconds
(without alignments)
1539.164 Million cell updates/sec

Title: US-10-650-369-12

Perfect score: 1715

Sequence: 1 MVKVGINGFGRIGRLAFRR.....EMSYTAQLVRTLEYFAKIAK 336

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2833366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : PIR78:
1: PIR1,*
2: PIR2,*
3: PIR3,*
4: PIR4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99.8	336	2	A42963	glyceraldehyde-3-P
2	94.3	336	2	S71350	glyceraldehyde-3-P
3	92.9	335	2	F95235	glyceraldehyde-3-P
4	92.9	359	2	G98099	glyceraldehyde-3-P
5	92.5	336	2	F86910	hypothetical protein
6	78.0	336	2	G86694	hypothetical protein
7	75.2	334	2	S34254	glyceraldehyde-3-P
8	73.6	336	2	AC1382	glyceraldehyde-3-P
9	73.5	336	2	AD1751	glyceraldehyde-3-P
10	73.4	334	2	C96987	glyceraldehyde-3-P
11	69.8	334	2	BB2019	glyceraldehyde-3-P
12	69.1	334	2	BB1001	glyceraldehyde-3-P
13	69.0	336	2	B98850	glyceraldehyde-3-P
14	60.3	58.5	338	T09633	glyceraldehyde-3-P
15	57.9	333	2	F90881	glyceraldehyde-3-P
16	57.9	333	2	F9737	glyceraldehyde-3-P
17	53.7	337	2	S73737	glyceraldehyde-3-P
18	53.0	336	2	A43260	glyceraldehyde-3-P
19	52.9	337	2	C64233	glyceraldehyde-3-P
20	52.9	349	2	F90517	glyceraldehyde-3-P
21	52.3	335	1	DEBSG	glyceraldehyde-3-P
22	52.0	335	2	S12696	glyceraldehyde-3-P
23	51.6	335	1	DEBSGP	glyceraldehyde-3-P
24	51.5	335	2	H84094	glyceraldehyde-3-P
25	51.0	333	1	DEHGTT	probable glyceraldehyde-3-P
26	50.3	335	2	A70107	glyceraldehyde-3-P
27	49.2	342	2	F70391	glyceraldehyde-3-P
28	49.1	336	2	T36020	glyceraldehyde-3-P
29	48.5	336	2	AI0262	glyceraldehyde-3-P

ALIGNMENTS

RESULT 1

A42963

Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Streptococcus

NI: Alternative names: plasmin receptor

CI: Species: Streptococcus sp.

CD: Date: 10-Mar-1994 #sequence revision 10-Mar-1994 #text_change 03-Jun-2002

CAccession: A42963; B42963; JH0750

R.Lottenberg, R.; Broder, C.C.; Boyle, M.D.; Kain, S.J.; Schroeder, B.L.; Curtiss III, F.J. Bacteriol. 174, 5204-5210, 1992

A:Title: Cloning, sequencing, analysis, and expression in Escherichia coli of a streptococcal

A:Reference number: A42963; PMID:92355491; MUID:1322883

A:Accession: A42963

A: Molecule type: DNA

A: Residues: 1-336 <LOT>

A: Experimental source: group A, strain 64/14

A: Note: sequence extracted from NCBI backbone (NCBIP:110308)

A:Accession: B42963

A: Molecule type: protein

A: Residues: 2-74,161-164,'X',166-174,187-211,'X',213-217 <LC2>

R.Pancholi, V.; Fischetti, V.A.

J. Exp. Med. 176, 411-426, 1992

A:Accession: JH0750

A: Molecule type: protein

A: Residues: 2-30...A...32-40 <PAN>

A:Accession: JH0750

A: Molecule type: protein

A: Residues: 2-30...A...32-40 <PAN>

A:Accession: JH0750

A: Molecule type: protein

A: Residues: 1-334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match 99.8%; Score 1711; DB 2; Length 336;

Best Local Similarity 99.4%; Pred. No. 4.2e-116;

Matches 334; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVKVINGFGRIGRAFRRIONVEVTRINDLTDPNMLAHLKRYDTTQGRFDGTYEV 60

DB 1 MYVKVINGFGRIGRAFRRIONVEVTRINDLTDPNMLAHLKRYDTTQGRFDGTYEV 60

QY 61 KEGGFTEYGNFIVKVSERDPNIDWATDGEVILATGFPAKKEAELHANGARKVVI 120

DB 61 KEGGFTEYGNFIVKVSERDPNIDWATDGEVILATGFPAKKEAELHANGARKVVI 120

QY 121 TAGGNNDVKTIVFNTHDGTTETVSGASCTTNGLAPAKALHDAPGIOKGLMTTIHA 180

DB 121 TAGGGNDVKTIVFNTHDGTTETVSGASCTTNGLAPAKALHDAPGIOKGLMTTIHA 180

QY 241 GSVTELVVUTLDKNSVDEINAMKAASNDSEGYTEDPIVSSDIVGSYGSILFDATQTKM 300

Db	241	GSVTELVVLDKNSVDEINAKASNDSEGYTDPIVSSDIVGSYGSLSFDATOTKVM	300	A;Status: Preliminary A;Molecule type: DNA A;Residues: 1-335 <KDR> A;Cross-references: GB:AE005672; PIDN:AAK76079.1; PID:914973522; GSPDB:GN00164; TIGR:SP:
Qy	301	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	336	C;Species: Streptococcus "equisimilis" C;Accession: S71350 C;Title: Cloning, sequencing and functional overexpression of the Streptococcus equisimilis inding protein. Purification and biochemical characterization of the protein. A;Reference number: S71350; MUID:96305364; PMID:8706717
Db	301	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	336	A;Molecule type: DNA A;Residues: 1-336 <GAS> A;Cross-references: EMBL:X97788; NID:gi478268; PIDN:CAA66377.1; PID:91478269 A;Experimental source: strain H46A C;Genetics:
RESULT 2				
Db	241	GSVTELVVLDKNSVDEINAKASNDSEGYTDPIVSSDIVGSYGSLSFDATOTKVM	300	A;Status: Preliminary A;Molecule type: DNA A;Residues: 1-335 <KDR> A;Experimental source: strain TIGR4 C;Genetics:
Qy	1	MYVKVINGFGRIGRAFRRIONVEGVEVTRINDTDPMNLALHKLKYDTTQGRFDGTVEV	60	A;Gene: SP2012 C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
Db	1	MYVKVINGFGRIGRAFRRIONVEGVEVTRINDTDPMNLALHKLKYDTTQGRFDGTVEV	60	A;Gene: SP2012 C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
Qy	1	KEGGFEYNGN7IKVSERDPENIDWATDGVIVLZTGFPAKKEAELKHANGAKKVKVI	120	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
Db	1	KEGGFEYNGKFKVVSERDPENIDWATDGVIVLZTGFPAKKEAELKH-L-KGGAKKVKVI	119	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
Qy	1	TAPGGNDVKTIVFNTNDILDGTETVSGASCTTNLAPAKALHAFGQKGLMTIHA	180	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
Db	1	TAPGGNDVKTIVFNTNDILDGTETVSGASCTTNLAPAKALHAFGQKGLMTIHA	179	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
Qy	1	YTGQDMILDGPHRGGLDRARAAGAANTVNSTGAAKAGIVTPELNGKLDAAQRYPVPT	240	Query Match Score 94.3%; Best Local Similarity 95.3%; Pred. No. 2.5e-109; Indels 0; Gaps 0; Mismatches 321; Conservative Matches 321; Conservative
Db	1	YTGQDMILDGPHRGGLDRARAAGAANTVNSTGAAKAGIVTPELNGKLDAAQRYPVPT	239	Query Match Score 94.3%; Best Local Similarity 95.3%; Pred. No. 2.5e-109; Indels 0; Gaps 0; Mismatches 321; Conservative Matches 321; Conservative
Qy	1	GSVTELVVLDKNSVDEINAKASNDSEGYTDPIVSSDIVGSYGSLSFDATOTKVM	300	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
Db	1	GSVTELVVLDKNSVDEINAKASNDSEGYTDPIVSSDIVGSYGSLSFDATOTKVM	299	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
Qy	1	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	336	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
Db	1	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	335	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.3e-107; Indels 1; Gaps 1;
RESULT 4				
Db	61	KEGGFEYNGNFIKVSERDPENIDWATDGVIVLZTGFPAKKEAELKHANGAKKVKVI	120	A;Status: Preliminary A;Molecule type: DNA A;Residues: 1-359 <KDR> A;Cross-references: GB:AE007317; PIDN:AAI00628.1; PID:915459513; GSPDB:GN00174
Qy	61	KEGGFEYNGNFIKVSERDPENIDWATDGVIVLZTGFPAKKEAELKHANGAKKVKVI	120	C;Species: Streptococcus pneumoniae C;Accession: G98099 C;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G98099 C;Keywords: glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [Imported] - S:
Db	121	TAPGGNDVKTIVFNTNDILDGTETVSGASCTTNLAPAKALHAFGQKGLMTIHA	180	C;Species: Streptococcus pneumoniae C;Accession: G98099 C;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G98099 C;Keywords: glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [Imported] - S:
Qy	121	TAPGGNDVKTIVFNTNDILDGTETVSGASCTTNLAPAKALHAFGQKGLMTIHA	180	C;Species: Streptococcus pneumoniae C;Accession: G98099 C;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G98099 C;Keywords: glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [Imported] - S:
Db	121	TAPGGNDVKTIVFNTNDILDGTETVSGASCTTNLAPAKALHAFGQKGLMTIHA	180	C;Species: Streptococcus pneumoniae C;Accession: G98099 C;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G98099 C;Keywords: glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [Imported] - S:
Qy	181	YTGQDMILDGPHRGGLDRARAAGAANTVNSTGAAKAGIVTPELNGKLDAAQRYPVPT	240	C;Species: Streptococcus pneumoniae C;Accession: G98099 C;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G98099 C;Keywords: glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [Imported] - S:
Db	181	YTGQDMILDGPHRGGLDRARAAGAANTVNSTGAAKAGIVTPELNGKLDAAQRYPVPT	240	C;Species: Streptococcus pneumoniae C;Accession: G98099 C;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6. A;Reference number: A97872; MUID:21429245; PMID:11544234 A;Accession: G98099 C;Keywords: glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) [Imported] - S:
Qy	241	GSVTELVVLDKNSVDEINAKASNDSEGYTDPIVSSDIVGSYGSLSFDATOTKVM	300	C;Species: Streptococcus pneumoniae C;Accession: F95235 C;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Accession: F95235
Db	241	GSVTELVVLDKNSVDEINAKASNDSEGYTDPIVSSDIVGSYGSLSFDATOTKVM	300	C;Species: Streptococcus pneumoniae C;Accession: F95235 C;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Accession: F95235
Qy	301	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	336	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;
Db	301	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	336	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;
Qy	1	MYVKVINGFGRIGRAFRRIONVEGVEVTRINDTDPMNLALHKLKYDTTQGRFDGTVEV	60	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;
Db	1	MYVKVINGFGRIGRAFRRIONVEGVEVTRINDTDPMNLALHKLKYDTTQGRFDGTVEV	59	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;
Qy	1	KEGGFEYNGNFIKVSERDPENIDWATDGVIVLZTGFPAKKEAELKHANGAKKVKVI	120	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;
Db	1	KEGGFEYNGKFKVVSERDPENIDWATDGVIVLZTGFPAKKEAELKH-L-KGGAKKVKVI	119	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;
Qy	1	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	336	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;
Db	1	EVDGSOLVKVVSYWDNEMSYTAQLVRTLEYFAKIAK	335	Query Match Score 92.9%; Best Local Similarity 92.6%; Pred. No. 1.4e-107; Indels 1; Gaps 1;

Qy 121 TAPGGNDVKTIVFNTNHDILDGTETVVISGASCTINCLAPMAKALHDAPFQKGIMTTIHA 180
 Db 144 TAPGGNDVKTIVFNTNHDILDGTETVVISGASCTINCLAPMAKALQDNFQVGEGLMTHA 203

Qy 181 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELINGKLDGAQORVPVPT 240
 Db 204 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELINGKLDGSQORVPVPT 263

Qy 241 GSVTELUVTLDKNSVDEINAMKAASNDSFQTYEDPVISSDTIVGVSIGSLSLFDATOTKVM 300
 Db 264 GSVTELUVTLDKNSVDEINAMKAASNEQTYEDPVISSDTIVGMSYSLFDATOTKVM 323

Qy 301 EVDGSOLVKVTVSYWDNEMSYTAQLVRTLEYFAKIAK 336
 Db 324 DVGKQLVKTVSYWDNEMSYTAQLVRTLEYFAKIAK 359

RESULT 5
 F86905 hypothetical protein gapB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C; Species: Lactococcus lactis subsp. lactis
 C; Accession: F86905
 R; Bolotin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis (strain IL1403)
 A; Reference: PMID:21235186; PMID:11337471
 A; Accession: F86905
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-336 <STO>
 A; Cross-references: GB:AE005176; PID:912723315; PID:AAK06344.1; GSPDB:GN00146
 A; Experimental source: strain IL1403
 C; Genetics:

A; Gene: gapB
 C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 78.0%; Score 1338.5; DB 2; Length 337;
 Best Local Similarity 77.2%; Pred. No. 3.2e-89;
 Matches 260; Conservative 31; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MVVKVINGFGRIGRLAARRIONVEGVEVTRINDLTDPMIAHLKLYDTTQGRFDGTVEV 60
 Db 1 MVKVINGFGRIGRLARRQEVGEVVAHINDLTDPMIAHLKLYDTTQGRFDGTVEV 60

Qy 61 KEGGFEYNGNFKVSAERDPENIDWATDGVIEVILPATGFFAKKEAELKHANGAKKVKVI 120
 Db 61 KEGGFDYNGKFKVTAERNPFDQWDSGVBIVLDTGGFFAKKEAELKHLPGGAKKVKVI 120

Qy 121 TAPGGNDVKTIVTENTHILDGTETVVISGASCTINCLAPMAKALHDAPFQKGIMTTIHA 180
 Db 121 TAPGGNDVKTIVTENTHILDGTETVVISGASCTINCLAPMAKALNPNFGYGGTMTVHS 180

Qy 181 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELINGKLDGAQORVPVPT 240
 Db 181 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELSGLMGHQAQRVSTPT 240

Qy 241 GSVTELUVTLDKNSVDEINAMKAASNDSFQTYEDPVISSDTIVGVSIGSLSLFDATOTKVM 300
 Db 241 GSVTELUVTLEYFAKIAKDEINAMKAASNDSFQTYEDPVISSDTIVGMSYSLFDATOTKVM 300

RESULT 7
 S34254 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Clostridium
 C; Species: Clostridium pasteurianum
 C; Accession: S34254
 R; Oster, T.; Assobhei, O.; Scherzer, S.; Branlant, G.; Branlant, C.
 C; Description: Nucleotide sequence of the glyceraldehyde-3-phosphate dehydrogenase from
 A; Reference number: S34254
 A; Accession: S34254
 A; Molecule type: DNA
 A; Residues: 1-34 <STO>
 A; Cross-references: EMBL:X72219; NID:911923; PID:CAAS1020.1; PID:911924
 C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 C; Genetics:

Query Match 82.2%; Score 1410; DB 2; Length 336;
 Best Local Similarity 81.2%; Pred. No. 2.2e-94;
 Matches 273; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

Qy 1 MVVKVINGFGRIGRLAARRIONVEGVEVTRINDLTDPMIAHLKLYDTTQGRFDGTVEV 60
 Db 1 MVVKVINGFGRIGRLAARRIONVEGVEVTRINDLTDPMIAHLKLYDTTQGRFDGTVEV 60

Qy 61 KEGGFEYNGNFKVSAERDPENIDWATDGVIEVILPATGFFAKKEAELKHANGAKKVKVI 120
 Db 61 KDGGEVNGNFKVTAESPNANIAEVREIVILEATGFFAKKEAELKHANGAKKVKVI 120

Qy 121 TAPGGNDVKTIVFNTNHDILDGTETVVISGASCTINCLAPMAKALHDAPFQKGIMTTIHA 180
 Db 121 TAPGGSDVKTIVFNTNHEVLDGTETVVISGASCTINCLAPMAKALNPKVGTMTVHG 180

Qy 181 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELINGKLDGAQORVPVPT 240
 Db 181 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELOGKQGHQORVPVPT 240

Qy 241 GSVTELUVTLDKNSVDEINAMKAASNDSFQTYEDPVISSDTIVGVSIGSLSLFDATOTKVM 300
 Db 241 GSVTELUVTLDKNSVDEINAMKAASNEQTYEDPVISSDTIVGMSYSLFDATOTKVM 300

Qy 301 EVDGSOLVKVTVSYWDNEMSYTAQLVRTLEYFAKIAK 336
 Db 301 SADGQLVKTVSYWDNEMSYTAQLVRTLEYFAKIAK 336

RESULT 6
 G86694 hypothetical protein gapA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C; Species: Lactococcus lactis subsp. lactis
 C; Date: 23-Mar-2001 #sequence revision 23-Mar-2001 #text_change 03-Aug-2001
 C; Accession: G86694
 R; Bolotin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli

Genome Res. 11, 731-753, 2001
 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis (strain IL1403)
 A; Reference number: A86622; MJD:21235186; PMID:11337471

A; Status: Preliminary

A; Molecule type: DNA

A; Residues: 1-337 <STO>

A; Cross-references: GB:AE005176; PID:912723346; PID:AAK04657.1; GSPDB:GN00146

A; Experimental source: strain IL1403

C; Genetics:

C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 78.0%; Score 1338.5; DB 2; Length 337;

Best Local Similarity 77.2%; Pred. No. 3.2e-89;

Matches 260; Conservative 31; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MVVKVINGFGRIGRLAARRIONVEGVEVTRINDLTDPMIAHLKLYDTTQGRFDGTVEV 60

Db 1 MVVKVINGFGRIGRLARRQEVGEVVAHINDLTDPMIAHLKLYDTTQGRFDGTVEV 60

Qy 61 KEGGFEYNGNFKVSAERDPENIDWATDGVIEVILPATGFFAKKEAELKHANGAKKVKVI 120

Db 61 KEGGFDYNGKFKVTAERNPFDQWDSGVBIVLDTGGFFAKKEAELKHLPGGAKKVKVI 120

Qy 121 TAPGGNDVKTIVTENTHILDGTETVVISGASCTINCLAPMAKALHDAPFQKGIMTTIHA 180

Db 121 TAPGGNDVKTIVTENTHILDGTETVVISGASCTINCLAPMAKALNPNFGYGGTMTVHS 180

Qy 181 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELINGKLDGAQORVPVPT 240

Db 181 YTGDQMLDGPGRGDLRARAAGANTVNPNSTGAKAIGLVIPELSGLMGHQAQRVSTPT 240

Qy 241 GSVTELUVTLDKNSVDEINAMKAASNDSFQTYEDPVISSDTIVGVSIGSLSLFDATOTKVM 300

Db 241 GSVTELUVTLEYFAKIAKDEINAMKAASNDSFQTYEDPVISSDTIVGMSYSLFDATOTKVM 300

Qy 301 EVDGSOLVKVTVSYWDNEMSYTAQLVRTLEYFAKIAK 336

Db 301 SADGQLVKTVSYWDNEMSYTAQLVRTLEYFAKIAK 336

RESULT 6
 G86694 hypothetical protein gapA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C; Species: Lactococcus lactis subsp. lactis

C; Date: 23-Mar-2001 #sequence revision 23-Mar-2001 #text_change 03-Aug-2001

C; Accession: G86694

R; Bolotin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli

Genome Res. 11, 731-753, 2001
 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis s.

A; Reference number: A86622; MJD:21235186; PMID:11337471

A; Status: Preliminary

A; Molecule type: DNA

A; Residues: 1-337 <STO>

A; Cross-references: GB:AE005176; PID:91272346; PID:AAK04657.1; GSPDB:GN00146

A; Experimental source: strain IL1403

C; Genetics:

C; Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 78.0%; Score 1338.5; DB 2; Length 337;

Best Local Similarity 77.2%; Pred. No. 3.2e-89;

Matches 260; Conservative 31; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MVVKVINGFGRIGRLAARRIONVEGVEVTRINDLTDPMIAHLKLYDTTQGRFDGTVEV 60

Db 1 MTKVANGFGRIGRLARRQEVGEVVAHINDLTDPMIAHLKLYDTTQGRFDGTVEV 60

Qy 61 EGGFEYNGNFKVSAERDPENIDWATDGVIEVILPATGFFAKKEAELKHANGAKKVKVI 120

Db 61 EGGFDTYNGKFKVTAERNPFDQWDSGVBIVLDTGGFFAKKEAELKHLPGGAKKVKVI 119

Qy 121 EVDGSOLVKVTVSYWDNEMSYTAQLVRTLEYFAKIAK 336

Db 122 APGGNDVKTIVTENTHILDGTETVVISGASCTINCLAPMAKALHDAPFQKGIMTTIHA 181

RESULT 8

AC1382

glyceraldehyde 3-phosphate dehydrogenase homolog [Imported] - *Listeria* monocytophaga

C;Species: *Listeria* monocytophaga

C;Accession: AC1382

C;Sequence_revision: 27-Nov-2001 #text_change 14-Dec-2001

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jonsze, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.

A;Title: Comparative Genomics of *Listeria* species

A;Reference number: AB1077; MUID:21337279; PMID:11679669

A;Accession: AD1751

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-336 <GLA>

A;Cross-references: GB:AL592022; PIDN:CAC97780.1; PID:916415075; GSPDB:GN00178

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: gap

C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 73.5%; Score 1261; DB 2; Length 336;

Best Local Similarity 73.3%; Pred. No. 1.3e-83;

Matches 247; Conservative 32; Mismatches 56; Indels 2; Gaps 2;

Qy 1 MVKVKGNGFGRIGRLAARRRQVEVTRINLDTPNMLAHLLKTYDTTQGRFDGTVEV 60

Db 1 MTKVKGNGFGRIGRLAARRRQVEVVAINDLTAKMLAHLLKTYDTTQGRFDGVEEV 60

Qy 61 KEGGFEVNGNFIKVSARDPENIDWATDGVETVLEATGFFAKAEAKHLHANGAKKVV 120

Db 61 HDGFFNTYNGKEYVTLVANPEELPGDILGVDFLCTGGFTAQDKAELHKA-GAKKVV 119

Qy 121 TAPGGNDVKTIVVNTNDILDGTTETVSGASCTTNCLAPMAKALHDAGIQLGMLTTIHA 180

Db 121 YTDGQMLDGHPRGGDLRARRAGAAANTVPSGAAKAGLIVIPELNGKLDDGAAQRPVPT 240

Qy 180 YTDGQNTLDAHPKGDFRARAENTPNNTGAAKAGIQLVPLTGKLDGAAQRPVPT 239

Db 180 SAPATGDKMTIVVNNTEDLGTTETVSGASCTTNCLAPMAKVLDEKPGVVEGLMLTTIHA 179

Qy 181 YTSDQMLDGHPRGGDLRARRAGAAANTVPSGAAKAGLIVIPELNGKLDDGAAQRPVPT 240

Db 180 SAPATGDKMTIVVNNTEDLGTTETVSGASCTTNCLAPMAKVLDEKPGVVEGLMLTTIHA 179

Qy 241 GSUTELVTLDKRVSDEINAMKAASN-DSFGCYTETDPIVSSDIDGVSYGSFLDFTQTKV 299

Db 240 GSUTELVTLDKRVTVDENAMEAASDPETFGTSDQVVSDDIKNTFGSLFDEFTQTKV 299

Qy 300 MEVDGSQIUVKVSWDNEMSTAQLVRLTEYFAKIAK 336

Db 300 LTVGDDQQLVKTVAWYDNEMSTAQLVRLTEYFAKIAK 336

RESULT 10

C96987

glyceraldehyde 3-phosphate dehydrogenase, gene gapC [Imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001

C;Accession: C96987

R;Nolling, J.; Breton, G.; Omelichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, R.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J; Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1c

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: C96987

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-334 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK78686.1; PID:915023589; GSPDB:GN00168

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC0709

C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 73.4%; Score 1259.5; DB 2; Length 334;

Best Local Similarity 71.9%; Pred. No. 1.6e-53;

Matches 241; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

RESULT 9

AD1751

glyceraldehyde 3-phosphate dehydrogenase homolog gap [imported] - *Listeria* innocua (strain)

C;Species: *Listeria* innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

Qy	2 VVKVINGPGRIGLAFRIKQVNVGEGVTRINDLTDPMMLAHLYDTTQGRFDGTEVEK 61 1 MAKAINFGGRIGLARILRILEVPGLEVAINDLTDKMLAHLYDKSSQRFNGEIEVK 60	Db	300 TVGGKQLVKIVAWYDNEMSYTCAQIVRTLEYFA 331
Qy	62 EGGFBEVGNFIVKUSAERDPENIDWATGVEIVLEATGFFAKKEAERHLHANGAKKVVIT 121 61 EGATVNGKEVKVFAADEPEKLGFDLIDVVECTGFTKGEKAHZHVRA-GAKKVV 119	Db	RESULT 12 Glyceraldehyde-3-phosphate dehydrogenase [Imported] - <i>Neisseria meningitidis</i> (strain E81001 C;Species: <i>Neisseria meningitidis</i> C;Date: 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: E81001 R;Tectellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.J.; Hickey, B.K.; Raft, D.L.; White, O.; Doughtery, B.A.; Pough, M. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.;
Qy	122 APGGNDVTKVVENTHDLIDGTETVSGASCNTCLAPMAMAKLHDAGFIQKGLMTTHAY 181 120 APAGNDLAKTIVENVNEDIDGTETVSGASCNTCLAPMAMKLNDEKIEKGFMTHAF 179	Db	Science 287, 1809-1815, 2000 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of <i>Neisseria meningitidis</i> serogroup B strain MC58. A;Reference number: A81000; PMID:10710307 A;Accession: E81001 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-334 <TET> A;Cross-references: GB:AE002563; GB:AE002098; NID:97227405; PID:AAF42467.1; PMID:9722741 A;Experimental source: serogroup B, strain MC58 C;Genetics: A;Gene: NMB2159 C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
Qy	182 TGDQMILGSPHGDLRARRAGANTIPNSTGAKAAGLIVBIEBINGKLGDGAQRYPVPTG 241 180 TNDONTLDPSPHGDLRARRAAAVSQTIPNSTGAKAQSQTDLAGLGDGAQRYPVPTG 239	Db	Query Match 60.1%; Score 1184.5; DB 2; Length 334; Best Local Similarity 69.3%; Pred. No. 4.1e-78; Matches 230; Conservative 35; Mismatches 66; Indels 1; Gaps 1;
Qy	242 SVTBBLVTLTDKIVSYDEINAAMKAANSIDSFGYTEDPVSADVGINYGSFLDATLTKIVD 301 240 SITELVSVLKKVTVETNAAMKAADSFGYTEDPVSADVGINYGSFLDATLTKIVD 299	Db	QY 1 MVKVINGFGRIGLAFRIQNTGEGVTRINDLTDPMMLAHLYDTTQGRFDGTEV 60 1 MSIVKAINGFGRIGLAFRIKDHVRA-GAKKVVIT 121 61 KEGGFEVGNFIVKUSAERDPENIDWATGVEIVLEATGFFAKKEAERHLHANGAKKVVIT 120 61 KDDAIVNGKEVKVFAADEPEKLGFDLIDVVECTGFTKGEKAHZHVRA-GAKKVVIT 119
Qy	302 VDGSQVLKVWSVDNEMSYTCAQIVRTLEYFAIK 336 300 VNGSQLVKTAATWDNEMSYTCAQIVRTLEYFAIK 334	Db	QY 121 TAGPNDYKTVVVENTHNDLIDGTETVSGASCNTCLAPMAMAKLHDAGFIQKGLMTTHA 180 120 SAPGNDYKTVVYGVNODILGDSSTVSAASCNTCLAPMAAVLQKEFGVVEGLMTTHA 179 181 YTGDQMILGSPHGDLRARRAGANTIPNSTGAKAAGLIVBIEBINGKLGDGAQRYPVPT 240 180 YTGDONTLDPSPHGDLRARRAAAVSQTIPNSTGAKAQSQTDLAGLGDGAQRYPVAS 239
Qy	301 EVDGSQLVTVLTDKIVSYDEINAAMKAANSIDSFGYTEDPVSADVGINYGSFLDATLTKIVM 300 300 TVGGKQLVKIVAWYDNEMSYTCAQIVRTLEYFA 332	Db	QY 241 GSVTBLVTVLTDKIVSYDEINAAMKAANSIDSFGYTEDPVSADVGINYGSFLDATLTKIVM 300 240 GSLTELVSLPRTKEENANDKAAAESEYGNEDQIVSSDVGIEYGSFLDATLTKIVM 299
Qy	61 KEGGFEVGNFIVKUSAERDPENIDWATGVEIVLEATGFFAKKEAERHLHANGAKKVVIT 120 61 KDDAIVNGKEVKVFAADEPEKLGFDLIDVVECTGFTKGEKAHZHVRA-GAKKVVIT 119	Db	QY 301 EVDGSQLVTVLTDKIVSYDEINAAMKAANSIDSFGYTEDPVSADVGINYGSFLDATLTKIVM 300 300 TVGGKQLVKIVAWYDNEMSYTCAQIVRTLEYFA 332
Qy	121 TAGPNDYKTVVVENTHNDLIDGTETVSGASCNTCLAPMAMAKLHDAGFIQKGLMTTHA 180 120 SAPGNDYKTVVYGVNODILGDSSTVSAASCNTCLAPMAAVLQKEFGVVEGLMTTHA 179 181 YTGDQMILGSPHGDLRARRAGANTIPNSTGAKAAGLIVBIEBINGKLGDGAQRYPVPT 240 180 YTGDONTLDPSPHGDLRARRAAAVSQTIPNSTGAKAQSQTDLAGLGDGAQRYPVAT 239	Db	RESULT 13 Glyceraldehyde-3-phosphate dehydrogenase [Imported] - <i>Staphylococcus aureus</i> (strain N315 C;Species: <i>Staphylococcus aureus</i> C;Accession: E89850 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani, U.; Y., Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiota, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> . A;Reference number: A89758; PMID:21311952; PMID:11418146 A;Accession: E89850 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-33 <KUR> A;Cross-references: GB:BA000018; PID:913700663; PID:BA81960.1; GSPDB:GN00149 A;Protein: source: strain N315

C;Genetics:
 A;Gene: Gap
 C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase
 Query Match Similarity 69.0%; Score 1183; DB 2; Length 336;
 Best Local Similarity 68.2%; Pred. No. 5.3e-78;
 Matches 230; Conservative 43; Nsmatches 62; Indels 2; Gaps 2;
 Qy 1 MVVKVSIINGFGRIGLAFRRITQNVGEVETRINDLTPNMLAHILKYDTQGEGTVEV 60
 Db 1 NAVKVAINGFGRIGLAFRRQEVGLEYAVNDLDDMLAHILKYDTMQRFTGEVEV 60
 Qy 61 KEGGFEVNGNPKIVSAERDPENIDWATDGEVIEVILEATGFFAKKAAEKLHANGAKKVV 120
 Db 61 VDGGERVNGKREVKFSBPASKLPKNDLIVVLECTGFTDKOKAQAHTEA-GAKKVL 119
 Qy 121 TAPGGNDVKTIVYENTHDIDLTGTERVSIAGASCTTCNCLAPMAKALHDAFGIQKGMITIHA 180
 Db 120 SAPATEDLKVTTENTHDIDLTGTERVSIAGASCTTCNCLAPMAKALHDAFGIQKGMITIHA 179
 Qy 181 YTGDDQMLDGPGRGGDLRARRAGAAANTIPNISTGAAKAIIVIPBINGKLDGAAQQRVPVPT 240
 Db 180 YTGDDQMLDGPGRGGDLRARRAGAAANTIPNISTGAAKAIIVIPBINGKLDGAAQQRVPVPT 239
 Qy 241 GSVTELVYTLDK-NVSYDEINAAMKAASNDSEFGTYEDPFISSDPIVGYSVGSLSFDATQTKV 299
 Db 240 GSLTELVYTLDKQDVTVEYNEAMKNAESNEFGTYEDPFISSDPIVGYSVGSLSFDATQTKV 299
 Qy 300 MEVDGSQLQVTVSWTDNEMSVTAQLVRLTVEYPAKAK 336
 Db 300 MSVGDROLVKVAAWTDNEMSVTAQLVRLTVEYPAKAK 336

RESULT 15
 F90881 glyceraldehyde 3-phosphate dehydrogenase C [Imported] - Escherichia coli (strain O157:H7)
 C;Species: Escherichia coli
 C;Accession: F90881
 R: Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Nagasawa, N.; Yasunaga, T.; Khara, S.; Shiba, T.; Hatori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and Genbank
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-333 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BA835445;1; PID:913361488; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrate RIMD 0509982
 C;Genetics:
 A;Gene: Ecs2022
 C;Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match Similarity 57.0%; Score 993; DB 24; Length 333;
 Best Local Similarity 59.3%; Pred. No. 2.7e-64;
 Matches 198; Conservative 54; Nsmatches 76; Indels 6; Gaps 5;

Qy 4 KYGNGFGRIGLAFRRIONV-EYEVTRINDLTDFNMLAHILKYDTTQGRFDTGTVKE 62
 Db 3 KYGNGFGRIGLAFRRIONV-EYEVTRINDLTDFNMLAHILKYDTTQGRFDTGTVKE 62
 Qy 63 GGFEVNGNPKIVSAERDPENIDWATDGEVIEVILEATGFFAKKAAEKLHANGAKKVVITA 122
 Db 63 DSLRVDGKSIAYAAEKAQNTPKWAKGAEIIVECFTYSAEKSQAHDA-GAKKVLISA 121
 Qy 123 PGNDYKTVVENTNHDIDLTETVSIAGASCTTCNCLAPMAKALHDAFGIQKGMITIHAYT 182
 Db 122 PAG-EMKTTVVKVNDTLDGNDTIVISVAGASCTTCNCLAPMAKALHDSGIEVGTMITIHAYT 180
 Qy 183 GDOQMLLGPGRGGDLRARRAGAAQQRVPVPTGS 242
 Db 181 GQQLSIVDGP-RGKDLRASRAAENIIPHTGAAKAIIVIPBINGKLDGAQQRVPVPTGS 239
 Qy 243 VTELVYTLDKQDVTVEYNEAMKNAASNDSEFGTYEDPFISSDPIVGYSVGSLSFDATQTKV 300
 Db 240 VTELVYTLDKQDVTVEYNEAMKNAASNDSEFGTYEDPFISSDPIVGYSVGSLSFDATQTKV 299

Query Match Similarity 58.7%; Score 1003; DB 2; Length 338;
 Best Local Similarity 58.7%; Pred. No. 5.2e-65;
 Matches 199; Conservative 45; Nsmatches 89; Indels 6; Gaps 3;

Qy 1 MVVKVSIINGFGRIGLAFRRITQNVGEVETRINDLTPNMLAHILKYDTQGEGF 56
 Db 1 MTKVIGNGFGRIGLAFRRIMDGEBTRDJEVVAINDLTTPAMAHILKYDTQGEGF 60

Qy 57 TVEVKEGGFEVNGNPKIVSAERDPENIDWATDGEVIEVILEATGFFAKKAAEKLHANGA 115
 Db 61 EVSATEDSLVVDGKCYRVAEPQAQNTIPWVYRNDGTDFTGTYISAKSQAHLDA-GA 119
 Qy 116 KKVVITAPGGNDVKTIVFNTNHDIDLTETVSIAGASCTTCNCLAPMAKALHDAFGIQKGM 175
 Db 120 KRVLISAPAGNDLKTIVSYNQDTLTADDTIVSAGSCTTCNLSLAPANANKEFQVGM 179

Qy 176 TTIIAYTGGQMLDGPGRGGDLRARRAGAAIVPNSTGAKAIGLVIPELNGKLDGAACR 235

Search completed: May 11, 2004, 16:49:49
 Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model 1

Run on: May 11, 2004, 16:42:06 ; Search time 18 Seconds
(without alignments)

Title: US-10-650-369-12

Perfect Score: 1715

Sequence: 1 MVVKVGINGFGRIGRLAARR.....EMSYTAQLVRTLEYAKIAK 336

Scoring table: BLOSUM62

GapOp 10.0 , GapExt 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post -processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : SwissProt_42.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1709	99.7	335	1 G3P_STRPY	P5067 streptococc
2	1705	99.4	335	1 G3P_STRPY	Q8K9M9 streptococc
3	1612	94.0	335	1 G3P_STREQ	Q5906 streptococc
4	1338	78.5	337	1 G3P_LACLA	P5287 lactococcus
5	1289	75.2	334	1 G3P_CLOPA	Q5939 clostridium
6	1259	73.4	334	1 G3P_CLOAB	Q52631 clostridium
7	1190	69.4	336	1 G3P1_STAEP	Q8C95 staphylococ
8	1183	69.0	336	1 G3P1_STAAM	Q9ZC5 staphylococ
9	1003	58.5	338	1 G3P_LACDE	Q3255 lactobacill
10	993	57.9	333	1 G3P3_BCO57	P5872 escherichia
11	992	57.8	333	1 G3P3_ECOLI	P33398 escherichia
12	921	53.7	337	1 G3P_XNCPCN	P75558 mycoplasma
13	908	53.0	334	1 G3P_CORG1	P0151 mycoplasma
14	908	52.9	337	1 G3P_MTCGE	P4743 mycoplasma
15	891.5	52.0	334	1 G3P1_BACSU	P09124 bacillus su
16	880.5	51.7	334	1 G3P_BACME	P23229 bacillus me
17	880.5	51.3	334	1 G3P_BACST	P00632 bacillus st
18	873	50.9	332	1 G3P_THEMEA	P17221 thermogoga
19	863	50.3	335	1 G3P_BORBU	P46395 borrelia bu
20	843	49.2	342	1 G3P_AQAE	067161 aquifex aeo
21	842.5	49.1	336	1 G3P_STRCO	Q92118 streptomyce
22	817	47.6	330	1 G3P1_SALTY	P24165 salmonella
23	816	47.6	339	1 G3P_MYCTU	006322 mycobacteri
24	815	47.5	339	1 G3P_MYCLE	P46713 mycobacteri
25	813	47.4	330	1 G3P_ECOLI	P063977 escherichia
26	807.5	47.1	339	1 G3P_HABIN	P44304 haemophilus
27	801	46.7	339	1 G3P_STRLCO	P94915 mycobacteri
28	794.5	46.3	337	1 G3P1_RHIBA	09336 rhizomucor
29	794	46.3	330	1 G3P_XTRYB	P10397 trypanosoma
30	787.5	45.9	336	1 G3P1_SCPHO	P78398 schizosacch
31	784.5	45.7	332	1 G3P_RALSO	P52394 ralstonia s
32	783.5	45.7	337	1 G3P_MONAN	P53330 monascus an
33	779.5	45.5	338	1 G3P_NETCR	P00361 thermus aqu

SEQUENCE FROM N.A.

SEQUENCE FROM N.A., AND SEQUENCE OF 1-73; 166-173 AND 186-216.

SEQUENCE FROM N.A.; STRAIN=64/14;

MEDLINE=92355491; PubMed=13228893;

Lottnerberg R., Broder C.C., Boyle M.D., Kain S.J., Schroeder B.L.,

Curtiss R. III; "Cloning, sequence analysis, and expression in Escherichia coli of a streptococcal plasmin receptor." J. Bacteriol. 174:5204-5210(1992).

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.; STRAIN=SF370 / ATCC 700294 / Serotype M1;

MEDLINE=211292684; PubMed=11292296;

Ferratti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Savorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R., "Complete genome sequence and comparative microarray analysis of serotype M1 strains of Streptococcus

RT pyogenes." Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.; STRAIN=MGSB232 / Serotype M18; MEDLINE=21227593; PubMed=1197108;

Smoor J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylla G.L., Sturdevant D.E., Ricklefs S.M., Borcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapoor V., Daly J.A., Veasy L.G., Musser J.M., "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks." Proc. Natl. Acad. Sci. U.S.A. 99:4658-4673 (2002).

SEQUENCE OF 1-11; 20-30; 103-128; 162-171 AND 199-215.

SEQUENCE OF 1-11; 20-30; 103-128; 162-171 AND 199-21

DE	(Plasminogen-binding protein)	(Plasmin receptor).	
GN	GAP OR PLR OR SPMP3_0201 OR SPS0107.		
OS	Streptococcus pyogenes (serotype M3).		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI TaxID:198466;		
[1]	RN	SEQUENCE FROM N.A.	
	RP	SEQUENCE FROM N.A.	
	RC	SEQUENCE FROM N.A.	
RX	RC	SEQUENCE FROM N.A.	
RX	STRAIN=MGS315 / Serotype M3;		
RX	MEDLINE=21133808; Pubmed=12222206;		
RX	MEDLINE=22683228; Pubmed=12799345;		
RX	Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y., Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.P., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.,		
RA	"Genome sequence of serotype M3 strain of Streptococcus A phage-encoded toxins, the high-virulence phenotype, and clone emergence";		
RA	Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).		
[2]	RN	SEQUENCE FROM N.A.	
RN	RP	SEQUENCE FROM N.A.	
RN	RC	SEQUENCE FROM N.A.	
RX	RC	SEQUENCE FROM N.A.	
RX	STRAIN=SS-1 / Serotype M3;		
RX	MEDLINE=21133808; Pubmed=12222206;		
RX	Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y., Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T., Hattori M., Hamada S.,		
RA	"Genome sequence of an M3 strain of Streptococcus Pyogens reveals a large-scale genomic rearrangement in invasive strains and new insights into phage evolution."		
RA	Genome Res. 13:1042-1055 (2003).		
CC	-1- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN (By similarity).		
CC	-1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NAD(+) = 3-phospho-D-glyceraldehyde 3-phosphate + NADH.		
CC	-1- PATHWAY: Second phase of glycolysis; first step.		
CC	-1- SUBUNIT: Homotetramer (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-1- SIMILARITY: Belongs to the Glycereraldehyde 3-phosphate dehydrogenase family.		
CC	DR	AE014140; AAC78808; 1;	
CC	DR	AP005141; BAC63302; 1;	
CC	DR	InterPro; IPR00173; GAP_dhydrogenase.	
CC	DR	InterPro; IPR006424; GAPDH-1.	
CC	PFam	PF00044; Spdh; 1.	
CC	DR	PF02800; Spdh; C. 1.	
CC	DR	PRINTS; PRO00071; GAPDH-1.	
CC	DR	TIGRFAMs; TIGR01534; GAPDH-1.	
CC	DR	PROSITE; PS00071; GAPDH; 1.	
CC	KW	GLYCOSYLATION; Oxidoreductase; NAD; Complete proteome.	
FT	INIT_MET	0 0 BY SIMILARITY.	
FT	BINDING	151 151 GLYCERALDEHYDE 3-PHOSPHATE (BY SIMILARITY).	
FT	ACT_SITE	178 178 ACTIVATES THIOL GROUP DURING CATALYSIS	
FT	SEQUENCE	335 AA; 35841 MW; 4DDB767382PF698 CRC64;	
Qy	2	VVKVGGFGRIGRLAFLRRTQVVEGVTRINDLTPNNMLAHLLKYDTQGRFDGTVEVK 61	99.4%; Score 1705; DB 1; Length 335;
Qy	1	VVKVGGFGRIGRLAFLRRTQVVEGVTRINDLTPNNMLAHLLKYDTQGRFDGTVEVK 60	99.4%; Score 1705; DB 1; Length 335;
Db	1	EGGFEGVNGNFKVSAERDPENIDWATGVEVLEATGFFAKKEAERGH-HANGAKKVIT 121	99.4%; Score 1705; DB 1; Length 335;
Qy	62	EGGFEGVNGNFKVSAERDPENIDWATGVEVLEATGFFAKKEAERGH-HANGAKKVIT 121	99.4%; Score 1705; DB 1; Length 335;

Db	61. EGGFEVNGNFIKVSAAERDPEINIDWATDGVIVILEATGFFAKKEAAEKLHHTNGAKKVVIT 120	FT INIT MET 0 0 BY SIMILARITY.
Qy	122. APGGNDVKTIVVNTNHDIDLGTEVIVSASCNTNCLAPMAKALHDAGF1QGLMLTTIAY 181	FT GLYCERALDEHYDE 3 - PHOSPHATE (BY SIMILARITY).
Db	121. APGGNDVKTIVVNTNHDIDLGTEVIVSASCNTNCLAPMAKALHDAGF1QGLMLTTIAY 180	FT ACT_SITE 178 ACTIVATES THIOL GROUP DURING CATALYSIS
Qy	182. TGDQMLDOPHRGGDLRARAAGANIVNSTGAAKAGLVIPELNGKLDGAQQRVPVPTG 241	FT (BY SIMILARITY).
Db	181. TGDQMLDOPHRGGDLRARAAGANIVNSTGAAKAGLVIPELNGKLDGAQQRVPVPTG 240	FT SEQUENCE 335 AA; 35739 MN; FETACPFED765346 CRC64;
Qy	242. SVEELVVTIDKNTVSDEINAMKAASNDSGFYTEDPIVSDIVGVSGLFDATQIKVME 301	Query Match 94.0%; Score 1612; DB 1; Length 335;
Db	241. SVEELVVTIDKNTVSDEINAMKAASNDSGFYTEDPIVSDIVGVSGLFDATQIKVME 300	Best Local Similarity 95.5%; Pred. No. 1.7e-104;
Qy	302. VDGSQLVKKVSWDNEMSYTAQIQLVRLTEYFAKIAK 336	Matches 320; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
Db	301. VDGSQLVKKVSWDNEMSYTAQIQLVRLTEYFAKIAK 335	Qy 2 VVKVGINGFRIGRAFERRIQVNGVEVTRINDLTDPMNLALHLLKYDTQGRFGTVYEVK 61
Qy	303. VDGSQLVKKVSWDNEMSYTAQIQLVRLTEYFAKIAK 336	Db 1 VVKVGINGFRIGRAFERRIQVNGVEVTRINDLTDPMNLALHLLKYDTQGRFGTVYEVK 60
Db	301. VDGSQLVKKVSWDNEMSYTAQIQLVRLTEYFAKIAK 335	Qy 62 EGGFEVNGNFIKVSAAERDPEINIDWATDGVIVILEATGFFAKKEAAEKLHHTNGAKKVVIT 121
Db	301. VDGSQLVKKVSWDNEMSYTAQIQLVRLTEYFAKIAK 335	Db 61 EGGFEVNGNFIKVSAAERDPEINIDWATDGVIVILEATGFFAKKEAAEKLHHTNGAKKVVIT 120
RESULT 3		
G3P STRBQ	STANDARD; PRT; 335 AA.	FT 122 APGGNDVKTIVVNTNHDIDLGTEVIVSASCNTNCLAPMAKALHDAGF1QGLMLTTIAY 181
ID - G3D STRBQ	STANDARD; PRT; 335 AA.	Db 121 APGGNDVKTIVVNTNHDIDLGTEVIVSASCNTNCLAPMAKALHDAGF1QGLMLTTIAY 180
AC Q59706;		Qy 182 TGDQMLDOPHRGGDLRARAAGANTVNSTGAAKAGIIVPELNGKLDGAQQRVPVPTG 241
DT 01-NOV-1997 (Rel. 35, Created)		Db 181 TGDQMLDOPHRGGDLRARAAGANTVNSTGAAKAGIIVPELNGKLDGAQQRVPVPTG 240
DT 01-NOV-1997 (Rel. 35, Last sequence update)		DE 242 SVTELVVTIDKNTVSDEINAMKAASNDSGFYTEDPIVSDIVGVSGLFDATQIKVME 301
DT 28-FEB-2003 (Rel. 41, Last annotation update)		Db 241 SVTELVVTIDKNTVSDEINAMKAASNDSGFYTEDPIVSDIVGVSGLFDATQIKVME 300
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)		Qy 302 VDGSQLVKKVSWDNEMSYTAQIQLVRLTEYFAKIAK 336
DE (Plasminogen-binding protein) (Plasmin receptor).		Db 301 VDGSQLVKKVSWDNEMSYTAQIQLVRLTEYFAKIAK 335
GAP OR GAPC.		
GN Streptococcus equisimilis.		
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC Streptococcus		
OC Streptococcus		
OX NCBI_TaxID=119602;		
RN [1]		
SEQUENCE FROM N.A.		
RP STRAIN=416A;		
RC MEDLINE=96305364; PubMed=8706717;		
RA Gase K.; Gase A.; Schirmer H.; Malke H.;		
RT "Cloning, sequencing and functional overexpression of the		
RT streptococcus equisimilis R46A gapC gene encoding a		
RT glyceraldehyde-3-phosphate dehydrogenase that also functions as a		
RT plasminogen-binding protein. Purification and biochemical		
RT characterization of the protein.".		
RT Eur. J. Biochem. 239:42-51 (1996).		
CC -!- FUNCTION: ALSO BINDS HUMAN PLASMINOGEN.		
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +		
CC -!- NAD(+) = 3-phospho-D-glyceraldehyde 3-phosphate + NADH.		
CC -!- PATHWAY: Second phase of glycolysis; first step.		
CC -!- SUBUNIT: Homotrimer (By similarity).		
CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate		
CC dehydrogenase family.		
CC		
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CC		
CC		
CC		
EMBL: X97788; CAA6377.1; -.		
EMBL: Y12602; CAA3174.1; -.		
DR InterPro; IPR00113; GAP dhydrogenase.		
DR InterPro; IPR006424; GAPDH-1.		
PFam; PF00044; Spdh; 1.		
PFam; PF02800; Spdh_C; 1.		
PRINTS; PRO0078; G3PDHORGNASE.		
TIGRFAMS; TIGR0154; G3PDH-1.		
PROSITE; PS00071; GAPDH; 1.		
DR Glycolysis; Oxidoreductase; NAD.		
CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate		
CC dehydrogenase family.		
CC		
RESULT 4		
G3P_LACLA		
ID G3P_LACLA		
AC P52977;		
DT 01-OCT-1996 (Ref. 34, Created)		
DT 16-OCT-2001 (Ref. 40, Last sequence update)		
DT 28-FEB-2003 (Ref. 41, Last annotation update)		
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).		
DE GAP OR LI0559.		
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).		
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.		
OC NCBI_TaxID=1360;		
RN [1] - TaxID=1360;		
RP SEQUENCE FROM N.A.		
RC STRAIN=Lm2230;		
RX MEDLINE=95291425; PubMed=7773380;		
RA Canchiller M.R.; Hillier A.J.; Davidson B.E.;		
RA "Lactococcus lactis Glyceraldehyde-3-phosphate dehydrogenase gene, RT gap: further evidence for strongly biased codon usage in glycolytic		
RT Pathway genes."		
RT Microbiology 141:1027-1036 (1995).		
RN [2]		
RP SEQUENCE FROM N.A.		
RC STRAIN=Lm1403;		
RX MEDLINE=21235186; PubMed=11337471;		
RA Boloquin A.; Wincker P.; Mauger S.; Jaiillon O.; Malarme K.,		
RA Weissenbach J.; Ehrlich S.D.; Sorokin A.;		
RT "The complete genome sequence of the lactic acid bacterium Lactococcus		
RT lactis subsp. lactis IL1403."		
RT Genome Res. 11:731-753 (2001).		
RT Canchiller M.R.; Hillier A.J.; Davidson B.E.;		
RT "Lactococcus lactis Glyceraldehyde-3-phosphate + phosphate +		
RT NAD(+) = 3-Phospho-D-glyceraldehyde 3-phosphate + NADH.		
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +		
CC Pfam; PF00044; Spdh; 1.		
CC Pfam; PF02800; Spdh_C; 1.		
CC PRINTS; PRO0078; G3PDHORGNASE.		
CC TIGRFAMS; TIGR0154; G3PDH-1.		
CC PROSITE; PS00071; GAPDH; 1.		
CC Glycolysis; Oxidoreductase; NAD.		
CC -!- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate		
CC dehydrogenase family.		
CC		

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 CC or send an email to license@isb-sib.ch).

CC EMBL; L36907; AAC4153.1; -.
 DR PROSITE; PS00071; GAPDH; FALSE.
 DR PROSITE; PS00078; G3PDH; NEG.
 DR PRINTS; PR00078; G3PDH; NEG.
 DR PROSITE; PS00071; GAPDH; FALSE.
 DR GLYCOLYSIS; Oxidoreductase; NAD; Complete proteome.
 DR GLYCOLYSIS; Glyceraldehyde 3-phosphate
 DR BINDING 152 (BY SIMILARITY).
 DR ACT_SITE 179 179 ACTIVATES THIOL GROUP DURING CATALYSIS
 DR CONFLICT 143 143 (BY SIMILARITY).
 DR SEQUENCE 337 AA; 36057 MW; 17BB8C56AEEFF589D CRC64;

Query Match 78.0%; Score 1338.5; DB 1; Length 337;
 Best Local Similarity 77.2%; Pred. No. 1.4e-85;
 Matches 260; Conservative 31; Mismatches 45; Indels 1; Gaps 1;

Qy 1 MVVKVQINGFGRIGRLAERRRQVVEYTRINDLTDPMNLHILKYYDTQGRFDGTVE 60
 Db 1 MVVKVQINGFGRIGRLRRIQEVGVEVAHINDLTDPMNLHILKYYDTQGRFKGTVE 60
 Qy 61 KEGGFEVNGNPKIVSAERDPENIDRATDGVIEVILEATGFFAKKBAEAKHLHANGAKKVV 120
 Db 61 KEDGFDVNGKEFKVTABRNPEDIQWADSGVIEVILEATGFFAKKBAEAKHLHPGAKKVV 120
 Qy 121 TAPGNDVKTQVTFNTNHDLDGTETVSIQASCTINCLAMAKALHDAFGIOKGLIMITHA 180
 Db 121 TAPGNDVKTQVTFNTNHDLDGTETVSIQASCTINSLAMADALNKNPQVKGFTMTVHS 180
 Qy 181 YTGDQMLDGHFGGDLRARAQAGANTIPNSTGAKAIGLIVIPLNGKDGAAQRVPVPT 240
 Db 181 YTGDQMLDGHFGGDLRARAQAGANTIPNSTGAKAIGLIVIPLNGKDGAAQRVPVPT 240
 Qy 241 GSVTELVTVLDPKNSVDEINAMKASNSFGTYEDPIVSDIVGVSYSLSFDATOTKVM 300
 Db 241 GSITELVTVLDPKNSVDEINAMKASNSFGTYEDPIVSDIVGVSYSLSFDATOTKVM 300
 Qy 301 EV-DGSQLVKVWSWDNEEMSYTAQVRLTLEYFAKIAK 336
 Db 301 DLKDGGQLVKTAATWDNEMSFTAQLIRTLEYFAKIAK 337

RESULT 5
 G3_P_CLOPA STANDARD; PRT; 334 AA.
 AC 059319;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 17-FEB-2003 (Rel. 41, Last annotation update)
 DB Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH) (CP
 DB 17/CP 18).
 GN Clostridium pasteurianum.
 OS Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC [1] NCBI_TaxID=1501;
 RN SEQUENCE FROM N.A.
 RP

RA Oster T., Assobhei O., Scherrer S., Branlant G., Branlant C.;
 RL Submitted (JUN-1993) to the EMBL/GenBank/DDJB databases.
 RN [2]
 RP PARTIAL SEQUENCE OF 1-26.
 RC STRAIN=WS;
 RX MEDLINE=98231870; PubMed=9629918;
 PA Flengsrød R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";
 RL Electrophoresis 19:802-806 (1998).
 CC -|- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD (+) = 3-phospho-D-glyceroyl phosphate + NADH.
 CC -|- PATHWAY: Second phase of glycolysis; first step.
 CC -|- SUBUNIT: Homotetramer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cyttoplasmic.
 CC -|- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 CC dehydrogenase family.
 CC -----
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 CC -----
 DR EMBL; X72219; Q8A51020.1; -.
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
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 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
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 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
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 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
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 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
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 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
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 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
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 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
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 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
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 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
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 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
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 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
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 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
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 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
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 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
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 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
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 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS.
 DR SEQUENCE 334 AA; 36078 MW; D1505DODA7F2E27 CRC64;
 DR PIR; S34254; S34254.
 DR HSPP; P00324; 1GDI.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR InterPro; IPR000424; GAPDH-I.
 DR Pfam; PF00044; gpdh.
 DR Pfam; PF02800; gpdh_C.
 DR PRINTS; PR00078; G3PDH; G3PDH_NASE.
 DR TIGRFANS; TIGR01534; GAPDH-I.
 DR PROSITE; P00071; GAPDH; 1.
 DR GLYCOLYSIS; Oxidoreductase; NAD.
 DR FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE.
 DR ACT_SITE 177 177 ACTIVATES THIOL GROUP DURING CATALYSIS

AC	OS52631; DT16-OCT-2001 (Rel. 40, Created) DT16-OCT-2001 (Rel. 40, Last sequence update) DT28-FEB-2003 (Rel. 41, Last annotation update) Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH). GAP OR GPCP OR CAC0709; Clostridium acetobutylicum; Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium; NCBI_TaxID=1488; OXRN	SEQUENCE FROM N.A., AND CHARACTERIZATION. STRAIN=ATCC 824 / DSM 792 / VRM B-1787; MEDLINE=99392446; PubMed=10163150; Schreiber W., Durrie P.; "The Glyceraldehyde-3-phosphate dehydrogenase of Clostridium acetobutylicum: Isolation and purification of the enzyme, and sequencing and localization of the gap gene within a cluster of other glycolytic genes"; Microbiology 145:1839-1847(1999). [12] SEQUENCE FROM N.A. STRAIN=ATCC 824 / DSM 792 / VRM B-1787; MEDLINE=21359325; PubMed=11466286; Noelling J., Bretton G., Omechenko M. V., Makarova K. S., Zeng Q., Gibson R., Lee H. M., Dubois J., Qiu D., Hitti J., Wolfe Y. I., Tatusov R. L., Sabaté F., Boucette-Stamm L., Soucaille P., Daly M. J., Bennett G. N., Koonin E. V., Smith D. R., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.", J. Bacteriol. 183:4823-4838 (2001). -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH. -1- PATHWAY: Second phase of glycolysis; first step. -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
QY	122 APGGNDKVKTVVENTNHDILDGTETWISGASCTTCNCLAPAKAKLHDAGFIOKGLMTTHAY 181 120 APAGNDLKTIVENVNNDLDGTETWISGASCTTCNCLAPAKVNLNDKFGIEKGFMNTTHAP 179	122 APGGNDKVKTVVENTNHDILDGTETWISGASCTTCNCLAPAKAKLHDAGFIOKGLMTTHAY 181 120 APAGNDLKTIVENVNNDLDGTETWISGASCTTCNCLAPAKVNLNDKFGIEKGFMNTTHAP 179
DB	182 TGDONILDSPHRGEDLRRAGANTIPNSTGAKAIGVILPEINGKLGDGAQRYPVPTG 241 180 TNDQNTLDPHKGDLRRARAAVSTIPNSTGAKAISQVPLAGKLGDGAQRYPVPTG 239	182 TGDONILDSPHRGEDLRRAGANTIPNSTGAKAIGVILPEINGKLGDGAQRYPVPTG 241 180 TNDQNTLDPHKGDLRRARAAVSTIPNSTGAKAISQVPLAGKLGDGAQRYPVPTG 239
QY	242 SYTBLVVTLDKNSVDEIAAMKASANDSFQYTEDPIVSSDIVSYGSLFDATQKME 301 240 SIEBLVSVKKRKTVEEIAAMKAEADESFQYTEDPIVSDVVGINYGSLFDATLKVID 299	242 SYTBLVVTLDKNSVDEIAAMKASANDSFQYTEDPIVSSDIVSYGSLFDATQKME 301 240 SIEBLVSVKKRKTVEEIAAMKAEADESFQYTEDPIVSDVVGINYGSLFDATLKVID 299
DB	302 VDGSQLVKTWSWYDNEMSYTAQLYRTLEYFAKTAK 336 300 VNGSQLVTAAWYDNEMSYTSQLYRTLEYFAKTAK 334	302 VDGSQLVKTWSWYDNEMSYTAQLYRTLEYFAKTAK 336 300 VNGSQLVTAAWYDNEMSYTSQLYRTLEYFAKTAK 334
QY	RESULTS 7 G3P1 STAEF ID -G3P1 STAEF AC Q8CY5; DT 15-MAR-2004 (Rel. 43, Created) DT 15-MAR-2004 (Rel. 43, Last sequence update) DT 15-MAR-2004 (Rel. 43, Last annotation update) DE Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.1.12) (GAPDH 1). GN GAPAO OR GAP OR SB0557 OS <i>Staphylococcus epidermidis</i> . OC Bacteria; Firmicutes; Bacillales; <i>Staphylococcus</i> . RN NCBITaxonID=1282; RN [1] RP SEQUENCE FROM N.A. RX STRAIN=ATCC 12228; RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; RA "Genome-based analysis of virulence genes in a non-biofilm-forming RL <i>Staphylococcus epidermidis</i> strain (ATCC 12228)."; RL Mol. Microbiol. 49:1577-1583 (2003) CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + CC -1- NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH. CC -1- PATHWAY: Second phase of glycolysis; first step. CC -1- SUBUNIT: Homotrimer (By similarity). CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). CC -1- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family. CC -1- CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). CC -1- CC EMBL; AE016745; AAC004154; 1; CC PIR; C96987; C96388; 1; CC HSSP; P11772; 1HDC; CC InterPro; IPR000173; GAP_dhdrogenase. CC InterPro; IPR006424; GAPDH-1. CC Pfam; PF00044; Spdh; 1. CC PFAM; PF02800; Spdh; C. 1. CC PRINTS; PRO0078; G3PDHGRNASE. CC TIGR01534; G3PDHGRNASE. CC PROSITE; PS00077; GADDH; 1. CC KW Glycolysis; Oxidoreductase; NAD; Complete proteome. CC FT BINDING 150 151 CC ACT SITE 177 178 CC SEQUENCE 334 AA; 35850 MW; 1052A174B789B5 CRC64; CC 73.4% Score 1259.5; DB 1; Length 334; CC Best Local Similarity 71.9%; Prod. No. 4e-80; CC Matches 241; Conservative 40; Mismatches 53; Indels 1; Gaps 1; CC 2 VVKVGGNGFGRGLAARRIQTQVGEVTRINDLTDNMLAKYDQTQGRFDGTVK 61 CC 1 MARIATNGFGRGLAARRIYLEPGVAVTNDLDAKMLAKYDQTQGRFDGTVK 60 CC 62 EGGFEUNGFIKVSAAEDPENIDWATQGVIVLEATGFFAKKEAKHLHANGAKKVIT 121	
QY	151 151 DR InterPro; IPR006424; GAPdh-I. DR InterPro; IPR000173; GAP_dhdrogenase. DR PFAM; PF00044; Spdh; 1. DR PFAM; PF02800; Spdh; C. 1. DR PRINTS; PRO0078; G3PDHGRNASE. DR TIGR01534; G3PDHGRNASE. DR PROSITE; PS00077; GADDH; 1. DR KW Glycolysis; Oxidoreductase; NAD; Complete proteome. DR FT BINDING 151 151 DR ACT SITE 178 178 DR SEQUENCE 336 AA; 36190 MW; A962202D02AB5767 CRC64; DR 69.4% Score 1190; DB 1; Length 336;	151 151 DR InterPro; IPR006424; GAPdh-I. DR InterPro; IPR000173; GAP_dhdrogenase. DR PFAM; PF00044; Spdh; 1. DR PFAM; PF02800; Spdh; C. 1. DR PRINTS; PRO0078; G3PDHGRNASE. DR TIGR01534; G3PDHGRNASE. DR PROSITE; PS00077; GADDH; 1. DR KW Glycolysis; Oxidoreductase; NAD; Complete proteome. DR FT BINDING 151 151 DR ACT SITE 178 178 DR SEQUENCE 336 AA; 36190 MW; A962202D02AB5767 CRC64; DR 69.4% Score 1190; DB 1; Length 336;
DB	Query Match 2 Best Local Similarity 73.4% Score 1259.5; DB 1; Length 334; Matches 241; Conservative 40; Mismatches 53; Indels 1; Gaps 1;	Query Match 2 Best Local Similarity 73.4% Score 1259.5; DB 1; Length 334; Matches 241; Conservative 40; Mismatches 53; Indels 1; Gaps 1;

Best Local Similarity 69.4%; Pred. No. 2.5e-75; Matches 234; Conservative Matches 234; Mismatches 62; Indels 2; Gaps 2;

Qy 1 MVVKVINGFGRIGRARRRIVNVEVTRINDTDPNMLAHLKYDDTQGREDGTVY 60
 Db 1 MAIKVAVNGFGRIGRARRRIVDVEGEWAVNDTDDMLAHLKYDDTQGRTGEVY 60

Qy 61 KEGGFPEYGNPFTIKVSAERDPENIDWATDGVIVLEATGFAKERAEEKHLHANGAKKVV 120
 Db 61 TEGGFRTNGKEIKSFDEPDAGLPGDLDIDVLECTGFTDKERQAQHDA-GAKKVL 119

Qy 121 TAPGNDVVKTYFVNTHDILQETETVSGACTTNCALPAKALDAHDFQKGEMTTIA 180
 Db 120 SAPAKGKVKVTFVNTHDILQETETVSGACTTNSLAPAVKL-SDEFGLVEGEMTTIA 179

Qy 181 YTGDQMLDGFPRGGDLRARAAGANIVPSTGAKAIGLVIPENGKDGAAQRVPVFT 240
 Db 180 YTGDQMLDGFPRGGDLRARAAGANIVPSTGAKAIGLVIPENGKDGAAQRVPVFT 239

Qy 241 GSVTELTVLTDK-NVSVDTEINAAMKAANDSFGYTEDPIVSSDITGVSTGSLFDATQTV 299
 Db 240 GSVTELTVLTDKQDVTVQNSAMKAQDSEFGTYDEDIVSSDIVGTMGTSFLDATQTV 299

Qy 300 MEVDGSOVLUKVTVSWYDNEMSITAQLVRLTEYFAKAK 336
 Db 300 MTVGDRQVKVAAWYDNEMSITAQLVRLAHAAELSK 336

RESULT 8

G3P1_STAAM STANDARD: PRT; 336 AA.

AC Q925C5; Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Glyceraldehyde 3-phosphate dehydrogenase 1 (EC 1.2.1.12) (GAPDH 1).

GN GAP OR GAP OR SAV0772 OR MW0734.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699),

OS Staphylococcus aureus (strain N15),

OS Staphylococcus aureus (strain MW2), and

OC Staphylococcus aureus.

Bacteria; Firmicutes; Firmicutes; Bacillales; Staphylococcaceae.

NCBI_TAXID:158878, 158879, 196620, 1280;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=BB;

RA Morrissey J.A., Williams P.,

RT "Isolation and characterisation of a glycolytic operon in

RT Staphylococcus aureus.";

RT Submitted (MAR-1999) to the EMBL/GenBank/DBJU databases.

RN [2] SEQUENCE FROM N.A.

RP MEDLINE=21:11952; PubMed=1141146;

RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui J., Oguchi A., Aoki K.-I., Maruyama Y., Ito J.-O., Ito T.,

RA Kanamori M., Matsunari H., Murakami H., Hosoyama A.,

RA Mizutani-Ui Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kuhar S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogisawa N., Hayashi H., Hiramatsu K.,

RT "Whole genome sequencing of meticillin-resistant Staphylococcus

RT aureus.";

RT Lancet 357:1225-1240 (2001).

RN [3] SEQUENCE FROM N.A.

RC MEDLINE=22:040717; PubMed=12044378;

RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,

RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Chu L.,

RA Yamamoto K., Hiramatsu K.,

RT "Genome and virulence determinants of high virulence community-

RT acquired MRSA.";

RL Lancet 359:1819-1827 (2002).
 CC CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NADH.
 CC -|- NAD(+)= 3-phospho-D-glyceroyl phosphate + NADH.
 CC -|- PATHWAY: Second phase of glycolysis; first step.
 CC -|- SUBUNIT: Homotetramer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -|- SIMILARITY: Belongs to the Glyceraldehyde 3-phosphate dehydrogenase family.

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CC DR EMBL: AJ133520; CAB30645; 1; -
 DR EMBL: AP003360; BAB5634; 1; -
 DR EMBL: AP003131; BAB41960; 1; -
 DR EMBL: AP004824; BAB94599; 1; -
 DR PIR: E9850; E9850.
 DR SWISS-PROT; Q945C5; STAAAN.
 DR HSSP; P1772; 18DGS.
 DR InterPro; IPR006424; GAPDH_I.
 DR InterPro; IPR000173; GAP_dihydrogenase.
 DR Pfam; PF02800; SPdh_C; 1.
 DR PRINTS; PR00078; G3PDH_DRGNASE.
 DR TIGRANS; TIGR01534; GAPDH_I; 1.
 DR PROSITE; PS00071; GADDH; 1.
 KW Glyceraldehyde 3-phosphate (By similarity).
 FT GLYCOLYSIS; Oxidoreductase; NAD; Complete proteome.
 FT BINDING 151 ACTIVATES THIOL GROUP DURING CATALYSIS

FT ACT_SITE 178 (By SIMILARITY)
 FT SEQUENCE 336 AA; 36281 MW; 37ACCEA937677JB5 CRC64;
 SQ Query Match 69.0%; Score 1183; DB 1; Length 336;
 Best Local Similarity 68.2%; Pred. No. 7.9e-75; Mismatches 230; Conservative 43; Mismatches 62; Indels 2; Gaps 2;
 Qy 1 MVKVINGFGRIGRARRRIVNVEVTRINDTDPNMLAHLKYDTQGFDOTVEV 60
 DB 1 MAVKVAANGFGRIGRARRRIVNVEVTRINDTDPNMLAHLKYDTQGFDOTVEV 60
 Qy 61 KEGGFPEYGNPFTIKVSAERDPENIDWATDGVIVLEATGFAKERAEEKHLHANGAKKVV 120
 DB 61 VDGGPRVNGKEYKVSFEPDASKLPWDLNDIVLCTGFTDQKDAQHAKV 119
 Qy 121 TAPGNDVVKTYFVNTHDILQETETVSGACTTNCALPAKALDAHDFQKGEMTTIA 180
 DB 120 SAPATGDLKTVNTNHQELDSETVSGACTNSLAPVAKVLNDDFGLVEGLMTIHA 179
 Qy 181 YTGQMLDGPGRGDIIRRABAGANIVPNTGAKAIGVLPENGKLDGAAQRVPVET 240
 DB 180 YTGQMLDGPGRGDIIRRABAGANIVPNTGAKAIGVLPENGKLDGAAQRVPVAT 239
 Qy 241 GSYTETLVTLDK-NVSVDTEINAMKZASNSFGTTEPDIVSYGSLSFEDATQTKV 299
 DB 240 GSILTEITVLEQDVTEQVNEAMKASNSFGTTEPDIVSYGSLSFEDATQTRV 299
 Qy 300 MEVDGSSLVVKVTSWIDNEMSYTAQLVRLTEYFAKAK 336
 DB 300 MSVGRDQLVKYAAWYDNEMSYTAQLVRLAYLAELSK 336

RESULT 9

G3P_LACDE STANDARD; PRT; 338 AA.
 ID G3P_LACDE
 AC 032755;
 DT 16-Oct-2001 (Rel. 40, Created)
 DT 16-Oct-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
 GN GAP.
 OC Lactobacillus delbrueckii (subsp. bulgaricus).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OC NCBI_TaxID=1565;
 RN [1] _
 RP SEQUENCE FROM N.A.
 STRAIN=B107;
 RX MEDLINE=98240227; PubMed=9579064;
 RA Brann P., Delatorre P., Garei J.R.;
 "An operon encoding three glycolytic enzymes in Lactobacillus
 delbrueckii subsp. bulgaricus: glyceraldehyde 3-phosphate
 dehydrogenase, phosphoglycerate kinase and triosephosphate
 isomerase";
 RL Microbiology 144:905-914 (1998).
 CC |- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD (+) = 3-phospho-D-glycerate phosphate + NADH.
 CC |- PATHWAY: Second phase of glycolysis; first step.
 CC |- SUBUNIT: Homodotrimer (By similarity).
 CC |- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).
 CC |- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 dehydrogenase family.
 CC |-
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 or send an email to license@isb-sib.ch).
 CC |-
 EMBL; AU000339; CA04041.1; -.
 PIR; T09633; T09633.
 DR HSSP; P17721; 1HDG.
 DR InterPro; IPR000173; GAP dhydrogenase.
 DR InterPro; IPR006424; GAPDH-1.
 DR Pfam; PF00044; gapdh_1.
 DR Pfam; PF02800; gapdh_C_1.
 DR PRINTS; PRO0078; gapdhDHRGNASE.
 DR TIGRFAMS; TIGR01574; GAPDH-1.
 DR PROSITE; PS00071; GAPDH; FALSE NEG.
 KW Glycolysis; NAD; Oxidoreductase.
 FT BINDING 156 156 GLYCERALDEHYDE 3-PHOSPHATE
 (BY SIMILARITY).
 FT ACT_SITE 183 183 ACTIVATES THIOL GROUP DURING CATALYSIS
 (BY SIMILARITY).
 SQ SEQUENCE 338 AA; 36564 MW; D97889CA4F7DFA CRC64;
 Query Match 58 5% Score 1003; DB 1; Length 338;
 Best Local Similarity 58.7% Pred. No 2.2e-62;
 Matches 199; Conservative 45; Mismatches 89; Indels 6; Gaps 3;
 Qy 1 MVKVKGINGFGRIGRLAFLERRI---QNVGVETRINDTPNMLAHLYKDTTQGRFDG 56
 Db 1 MTKVKGINGFGRIGRLAFLERRIETVINDTPNMLAHLYKDTTQGRFDG 60
 Qy 57 TVEVKEGGFVNGNFIKVAERDPEIDVA-TDEEVTLEATGFFAKKEAEKLHANGA 115
 Db 61 EVSATEDSLVNDGKRYVVAEPQQNIPWVKNQDFVLETCIGFTYSSAKSQAHLDA-G 119
 Qy 116 KKVVITAPGGNDVKTIVFNTNHDIDGTTTIVSAGSCTTCLAPMALKHDAFGIQKGLM 175
 Db 120 KRVLISAPAGNDLKTIVSYNQDTLTADDTIVSAGSCTTSLAPMANLNGKFGIQVGT 179
 Qy 176 TTIIHAYTGDQMLDGFPHRGCDLRLRAGANITYPNSTGAKAAGLVLPELNGKLGQAQR 235
 Db 180 TTIIHAYTATOKVLDGPDGRNFRARAENLIPHSTGAKAAGLVLPELNGKLGQAQR 239
 Qy 236 VPVVPGNGSVTFLVLTIDKNUVSDEINAAMKAASNDSEGYTEDPIVSSDIVGYSGLFDAT 295
 Db 240 VPVVPGNGSVTFLVLTIDKNUVSDEINAAMKAASNDSEGYTEDPIVSSDIVGYSGLFDAT 299

Qy 296 QTRVMEVDGGSOLVKVSYWVSDNEWSYTAQVRLTLEYFAKI 334
 Db 300 QTRQVITAGDKLVLKTVTAWVNEYSEFCQWVRLHEATL 338

RESULT 10
 G3P3_ECO57 STANDARD; PRT; 333 AA.
 ID G3P3_ECO57
 AC P58072;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 RT Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12) (GAPDH-C).
 DE Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12) (GAPDH-C).
 GN GAPC OR 2230 OR ECG2022.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=8334;
 RN [1] _
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Blunkett G. III, Burland V., Mai B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
 RT RT
 RL DNA Res. 8:11-22 (2001).
 CC |- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
 CC NAD(+) = 3-Phospho-D-glyceroyl phosphate + NADH.
 CC |- PATHWAY: Second phase of glycolysis; first step.
 CC |- SUBUNIT: Homotrimer (By similarity).
 CC |- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC |- SIMILARITY: Belongs to the glyceraldehyde 3-phosphate
 dehydrogenase family.
 CC |-
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 or send an email to license@isb-sib.ch).
 CC |-
 DR EMBL; AB005364; AA56359_1; -.
 DR EMBL; AP002557; BA335445_1; -.
 DR PIR; C85737.
 DR PIR; F90881; F90881.
 DR HSSP; P17721; 1HDG.
 DR InterPro; IPR000173; GAP dhydrogenase.
 DR InterPro; IPR06424; GAPDH-1.
 DR Pfam; PF00044; gapdh_1.
 DR Pfam; PF0800; gapdh_C_1.
 DR PRINTS; PR00078; G3FDPHDRGNASE.
 DR TIGRFAMS; TIGR153; GAPDH-1.
 DR PROSITE; PS00071; GAPDH_1.
 KW Glycolysis; Oxidoreductase; NAD; Multigene family; Complete proteome.
 FT BINDING 150 150 GLYCERALDEHYDE 3-PHOSPHATE
 (BY SIMILARITY).

FT	ACT SITE	177	177	ACTIVATES THIOL GROUP DURING CATALYSIS
FT	SEQUENCE	333 AA;	35763 MW;	(BY SIMILARITY).
FT				A2F77CB2E773E64C CRC64;
Query	Query Match	57.9%;	Score 993;	DB 1; Length 333;
Query	Best local Similarity	59.3%;	Pred. No. 1; e-61;	Indels 6; Gaps :
Db	Matches 198; Conservative	54;	Mismatches 76;	Indels 6; Gaps :
Qy	4 KVGINGFGRIGRLAARRIONYE-GVEVTRINDLTDPMIHLALKYDITQGRDGTVEVK			
Db	3 KVGINGFGRIGRLVRLLEVKNSNIDVAINDLTSKILAYILKHDNSYGPWWSVDFIT			
Qy	63 GGEFEYNGNFKVSAERDPENIDWATGDEVETIATGFFAKKPEAAEKLHANGAKKVVIT			
Db	63 DSLIVGKSTAVAYEEAKAIPWKGAEITVBCGTYTSAKSQSAHDLA-GAKKVLIS			
Qy	123 PGGNDVKTIVWNTNHDILDGTETVIGSACSTINCLAPMAKALHDAGTQGKLMTTIHAY			
Db	122 PAG-EKTKTIVKVNDDTLIDGNDTIVSACSTINCLAMAKALHDGFTIEVGMTTHAY			
Qy	183 GDOMILDGPPIHGGDLRARAAGANIVPNSTGAKAIGLVIPELNGKLDGAQRPVPTG			
Db	181 GTQSLVDGP-RGKDRLRASRAAENIIPHTGTGAKAIGVIVIPELSKGKLGHAQRPVPTG			
Qy	243 VTELYVLTGKIVSVDEINAQKAA--ENDSFGTYEDPVVSSDIVGVSYGSLSLTDATQPKV			
Db	240 VTELVSTLGKVTAEVNNALQATINNESGFTYDEEVVSSDIIIGSHFGSVFEDATQPKV			
Qy	301 EYDGDSQVLYKIVSYWDNEMSYTAQOLVRLTLEYFAKL 334			
Db	300 AVGDLQLVKTVAWYDNEYGFVQLIRLTLEKFAKL 333			
RESULT 11				
G3P3_ECOLI	STANDARD; PRT; 333 AA.			
ID	G3P3_ECOLI			
AC	P33878; P76094; P78062; P78291; Q03855; Q63208;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Glyceraldehyde 3-phosphate dehydrogenase C (EC 1.2.1.12) (GAPDH-C).			
GN	GAPC OR B416/B417.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID:562;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-River isolate, and Clinical isolate;			
RC	STRAIN-K12;			
RC	MEDLINE=9722665; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"Escherichia coli" genes expressed preferentially in an aquatic environment;"			
RT	Mol. Microbiol. 28:325-332 (1998).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-K12 / MG1655;			
RC	MEDLINE=9722665; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12."			
SC	Science 277:1453-1474 (1997).			
RA	[3]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-K12 / MG1655;			
RC	MEDLINE=9722665; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12."			
SC	Science 277:1453-1474 (1997).			
RA	[4]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-K12;			
RC	MEDLINE=9722665; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12."			
SC	Science 277:1453-1474 (1997).			
RA	[5]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN-K12;			
RC	MEDLINE=9722665; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12."			
SC	Science 277:1453-1474 (1997).			
RA	[6]			

J. Bacteriol. 174:6076-6086 (1992).	Q4	P47543; [2]	SEQUENCE FROM N.A. (Rel. 33, Created) DT 01-FEB-1995 (Rel. 33, Last sequence update) DT 01-FEB-1995 (Rel. 41, Last annotation update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DT 28-FEB-2003 (Rel. 41, Last annotation update)
STRAIN=ATCC 13032 / DSM 2030 / NCIB 10025;	Db	"Complete genomic sequence of <i>Corynebacterium glutamicum</i> ATCC 13032." (EC 1.2.1.12) (GAPDH).	"Complete genomic sequence of <i>Corynebacterium glutamicum</i> ATCC 13032." (EC 1.2.1.12) (GAPDH).
Nakagawa S.	CC	Submitted (MAY 2002) to the EMBL/Genbank/DBJ databases	Mycoplasma genitalium.
- - CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NAD(+)	CC	- - CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NAD(+)	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
- - PATHWAY: Second phase of glycolysis; first step.	CC	- - PATHWAY: Second phase of glycolysis; first step.	NCBI_TaxID=209;
- - SUBUNIT: Homotrimer.	CC	- - SUBUNIT: Homotrimer.	RN
- - SUBCELLULAR LOCATION: Cytoplasmic.	CC	- - SUBCELLULAR LOCATION: Cytoplasmic.	SEQUENCE FROM N.A.
- - SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.	CC	- - SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.	STRAIN=ATCC 33330 / G-37; STRAIN=ATCC 33330 / G-37; STRAIN=ATCC 33330 / G-37; RX
EMBL; X59403; CAA2045.1; -	DR	EMBL; X59403; CAA2045.1; -	RX MEDLINE=960226346; PubMed=7569993;
PIR; APP05219; BAA98981.1; -	DR	PIR; APP05219; BAA98981.1; -	RX MEDLINE=9407520; PubMed=9253680;
PIR; A42260; A43260.	DR	PIR; A42260; A43260.	RX
HSSP; P00362; 1GDI.	DR	HSSP; P00362; 1GDI.	RA Fraser, C.M., Gocayne, J.D., White, O., Adams, M.D., Clayton, R.A., Kerlavage, A.R., Sutton, G., Kelley, J.M., Fleischmann, R.D., Bult, C.J., Karp, D., Kavallaris, M., Smith, K.V., Sandusky, M., Fuhrmann, J.L., Fritchman, J.L., Weismann, J.F., Small, D.M., Phillips, C.A., Merrick, J.M., Nguyen, D.T., Utterback, T.R., Saudek, D.M., Tomb, J.-F., Dougherty, B.A., Bott, K.F., Hu, P.-C., Lucier, T.S., Peterson, S.N., Smith, H.C., Hutchison, C.A. III, Venter, J.C., "The minimal gene complement of <i>Mycoplasma genitalium</i> ," Science 270:397-403 (1995).
InterPro; IPR0006434; GAPDH-I.	DR	InterPro; IPR0006434; GAPDH-I.	RA [1] - [2]
Pfam; PF00044; spdh, 1.	DR	Pfam; PF00044; spdh, 1.	RT "A survey of the <i>Mycoplasma genitalium</i> genome by using random sequencing,"
Pfam; PF02800; spdh, C, 1.	DR	Pfam; PF02800; spdh, C, 1.	RT "A survey of the <i>Mycoplasma genitalium</i> genome by using random sequencing,"
PRINTS; PR00078; G3FDHDGRNASE.	DR	PRINTS; PR00078; G3FDHDGRNASE.	RT "A survey of the <i>Mycoplasma genitalium</i> genome by using random sequencing,"
TIGRFAMS; TIGR01534; GAPDH-I.	DR	TIGRFAMS; TIGR01534; GAPDH-I.	RL J. Bacteriol. 175:7918-7930 (1993)
PROSITE; PS00071; GAPDH-I.	DR	PROSITE; PS00071; GAPDH-I.	CC - - CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate + NAD(+)
GLYCOBYSIS; Oxidoreductase; NAD; Complete proteome.	FT	GLYCOBYSIS; Oxidoreductase; NAD; Complete proteome.	CC NAD(+) = 3-Phospho-D-glyceroyl phosphate + NADH.
BINDING; 153	FT	BINDING; 153	CC PATHWAY: Second phase of glycolysis, first step.
ACT SITE; 180	FT	ACT SITE; 180	CC SUBUNIT: Homotetramer (By similarity).
CONFLICT; 25	FT	CONFLICT; 25	CC SUBCELLULAR LOCATION: Cytoplasmic.
SEQUENCE; 333 AA;	FT	SEQUENCE; 333 AA;	CC SIMILARITY: Belongs to the glyceraldehyde 3-phosphate dehydrogenase family.
Best Local Similarity 53.0%; Score 908; DB 1; Length 334; Matches 190; Conservative 41; Mismatches 94; Indels 13; Gaps 6;	CC	CC or send an email to license@ibb-sib.ch).	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Query Match 1 MVVKGFGGRIGRGLAFRRI-QNVEGVETRINLDPMMLAHLLKYDTTQGRFDGTV 59	Qy	1 MVVKGFGGRIGRGLAFRRI-QNVEGVETRINLDPMMLAHLLKYDTTQGRFDGTV 59	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Best Local Similarity 56.2%; Score 908; DB 1; Length 334; Matches 190; Conservative 41; Mismatches 94; Indels 13; Gaps 6;	Db	1 MTIRVINGFGRGRINFRFRLVRSRPLDGTQVTVLSDVLLVQV 60	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Query Match 1 VKEGGFEGVGNFIKSYAERPENPDWATGCVIILATGFFAKKEAEEKHLHANGAKKVV 119	Qy	1 VKEGGFEGVGNFIKSYAERPENPDWATGCVIILATGFFAKKEAEEKHLHANGAKKVV 119	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Best Local Similarity 61 YDDDSITVGSKRRIAYAERPKNLDWAANDIVLESTFFTDDAANAKAHIEA-GAKKVV 119	Db	1 YDDDSITVGSKRRIAYAERPKNLDWAANDIVLESTFFTDDAANAKAHIEA-GAKKVV 119	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Query Match 102 ITAPGGNDKVTCTVFTNTNHLD-GTETVSGASCTNCAPMAKALHDAFGIQKGLMTI 178	Qy	102 ITAPGGNDKVTCTVFTNTNHLD-GTETVSGASCTNCAPMAKALHDAFGIQKGLMTI 178	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Best Local Similarity 60 ISAPASNEADATEFVYGVHNSYDPHENHVNISGASCTTCNCLAPMAKLYNDKFGTENGMLTV 179	Db	102 ISAPASNEADATEFVYGVHNSYDPHENHVNISGASCTTCNCLAPMAKLYNDKFGTENGMLTV 179	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Query Match 61 HAYTGDQMLLDGPHRGDDLRARAGANVNPNSGAAKAIGLVLPELNGKLGDAAQRYPV 238	Qy	179 HAYTGDQMLLDGPHRGDDLRARAGANVNPNSGAAKAIGLVLPELNGKLGDAAQRYPV 238	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Best Local Similarity 180 HAYTGDQMLLDGPHRGDDLRARAGANVNPNSGAAKAIGLVLPELNGKLGDAAQRYPV 237	Db	180 HAYTGDQMLLDGPHRGDDLRARAGANVNPNSGAAKAIGLVLPELNGKLGDAAQRYPV 237	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Query Match 239 PTGSVTELVVTLDKRVSVDENNAANKAASDSFG ---TEDPVSSDVGVSGLSDPA 294	Qy	239 PTGSVTELVVTLDKRVSVDENNAANKAASDSFG ---TEDPVSSDVGVSGLSDPA 294	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Best Local Similarity 238 ITGSATDLTNTKSETVSINAKEAVGEGETLAVSEEPVLSVTDVLDHSDHSIFPDA 297	Db	238 ITGSATDLTNTKSETVSINAKEAVGEGETLAVSEEPVLSVTDVLDHSDHSIFPDA 297	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Query Match 295 TQTKYMEVDGSQVLRVSYDNEWSYTAOLVRLTLEYFA 332	Qy	295 TQTKYMEVDGSQVLRVSYDNEWSYTAOLVRLTLEYFA 332	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).
Best Local Similarity 298 GLTKV---SGNTVVKVSVTDNEWGTCOLLRLTEVVA 331	Db	298 GLTKV---SGNTVVKVSVTDNEWGTCOLLRLTEVVA 331	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).

Qy 242 SVTELVVTLDKNVSYDEINRANKAASNDS---FGYTEDPIVSSDIVGVSGLFDATQT 297
Db 239 SLVDIVAEINQEVTAEEVNLKEAEGDLKGILGYSEPLVSGDYNKNNSSTIDALST 298
Qy 298 KVMEVDGSQLYKUWSYDNEMSYTAQQLVTEPAK 333
Db 299 MVME---GSNKVKVISWYDNESGYSNRVWDLAAVIAK 331

Search completed: May 11, 2004, 16:48:17
Job time : 21 secs

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OM protein - Protein search, using SW model

Run on: May 11, 2004, 16:45:16 ; Search time 46 Seconds
 (without alignments)

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Title: US-10-650-369-12

Perfect score: 1715

Sequence: 1 MVVVKVINGFGRIGLAFR.....EMSYTAQLVRLTEYFAKTAK 336

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL25:*

1: SP_archaea:*

2: SP_bacteria:*

3: SP_fungi:*

4: SP_human:*

5: SP_invertebrate:*

6: SP_mammal:*

7: SP_rhinc:*

8: SP_organelle:*

9: SP_phage:*

10: SP_plant:*

11: SP_rodent:*

12: SP_virus:*

13: SP_vertebrate:*

14: SP_unclassified:*

15: SP_rvirus:*

16: SP_bacteriap:*

17: SP_archeap:*

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters:

1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL25:*

1: SP_archaea:*

2: SP_bacteria:*

3: SP_fungi:*

4: SP_human:*

5: SP_invertebrate:*

6: SP_mammal:*

7: SP_rhinc:*

8: SP_organelle:*

9: SP_phage:*

10: SP_plant:*

11: SP_rodent:*

12: SP_virus:*

13: SP_vertebrate:*

14: SP_unclassified:*

15: SP_rvirus:*

16: SP_bacteriap:*

17: SP_archeap:*

ALIGNMENTS

RESULT 1

Q83ZP7 ID Q83ZP7; PRELIMINARY;

AC Q83ZP7; ID Q83ZP7; PRELIMINARY;

DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Glyceraldehyde 3-P dehydrogenase.

GN

SP

Streptococcus dysgalactiae.

OS

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC

Streptococcus

NCBI TaxID:1334;

RN [1]

SEQUENCE FROM N.A.

RA Perez-Casal J.P., Bolton A., Song X.-M., Willison P., Potter A.A.;

RT "Use of the surface Proteins Gaps and Mgt of Streptococcus

RT dysalactiae as protective antigens against mastitis in non-lactating

SUMMARIES

Result No. Score Match Length DB ID Description

1 1715 100.0 336 2 Q83ZP7 Description

2 1618 94.3 336 2 Q8KVU6 Description

3 1609 93.8 336 2 Q9A1W2 Description

4 1619 93.8 336 16 Q833E8 Description

5 1619 93.8 336 16 Q8DXS8 Description

6 1593.6 93.1 336 2 Q8GER7 Description

7 1593.5 92.9 335 16 Q97NL1 Description

8 1593.5 92.9 359 16 Q8WN6 Description

9 1594 92.4 316 2 Q8KHG1 Description

10 1579.5 92.1 337 16 Q8DVV3 Description

11 1578 92.0 336 2 Q8KVU5 Description

12 1572 91.7 336 2 Q8VVB9 Description

13 1518 88.5 320 2 Q9LXK6 Description

14 1467.5 85.6 309 2 Q9A7T7 Description

15 1467.5 85.6 309 2 Q9A7T9 Description

16 1465.5 85.5 309 2 Q9A7T4 Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1 1715 100.0 336 2 Q83ZP7 Description

2 1618 94.3 336 2 Q8KVU6 Description

3 1609 93.8 336 2 Q9A1W2 Description

4 1619 93.8 336 16 Q833E8 Description

5 1619 93.8 336 16 Q8DXS8 Description

6 1593.6 93.1 336 2 Q8GER7 Description

7 1593.5 92.9 335 16 Q97NL1 Description

8 1593.5 92.9 359 16 Q8WN6 Description

9 1594 92.4 316 2 Q8KHG1 Description

10 1579.5 92.1 337 16 Q8DVV3 Description

11 1578 92.0 336 2 Q8KVU5 Description

12 1572 91.7 336 2 Q8VVB9 Description

13 1518 88.5 320 2 Q9LXK6 Description

14 1467.5 85.6 309 2 Q9A7T7 Description

15 1467.5 85.6 309 2 Q9A7T9 Description

16 1465.5 85.5 309 2 Q9A7T4 Description

Q9ajt5 streptococc
 Q9ajt6 streptococc
 Q9ajt7 streptococc
 Q9cdh4 lactococcus
 Q833i8 enterococcus
 Q84i4l listeria mo
 Q948h9 listeria in
 Q8XK79 clostridium
 Q8rfng fusobacteri
 Q9jvt8 neisseria m
 Q8bpys5 staphylococ
 Q83u3x3 neisseria g
 Q84hz6 neisseria g
 Q9jx95 neisseria m
 Q95c5 staphylococ
 Q94hz5 neisseria g
 Q9am61 staphylococ
 Q842r0 staphylococ
 Q84hz7 staphylococ
 Q8L2P7 staphylococ
 Q8L2P6 staphylococ
 Q8L2P8 staphylococ
 Q812r5 staphylococ
 Q8vm79 rhodospiril
 Q8L2R0 staphylococ
 Q8L2P7 staphylococ
 Q8L2P6 staphylococ
 Q8L2P8 staphylococ
 Q812r6 staphylococ
 Q812r7 staphylococ
 Q812r2 staphylococ

SEQUENCE FROM N.A.

RA Perez-Casal J.P., Bolton A., Song X.-M., Willison P., Potter A.A.;

RT "Use of the surface Proteins Gaps and Mgt of Streptococcus

RT dysalactiae as protective antigens against mastitis in non-lactating

RT cows."

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJU databases.

DR EMBL/AF315682; AP31408.1; -

DR GO:0004365; P glycolysis; IZB.

DR InterPro; IPR06424; GAPDH-1.

DR Pfam; PF00444; spdh; 1.

DR PRINTS; PRO0078; G3PDHDRGNAE.

DR TIGRFAMS; TIGR01534; GAPDH-1.

DR PROSTB; PS00071; GAPDH-1.

DR SEQUENCE 336 AA; 35528 MW; 1182B218CF037076 CRC64;

Query Match 100.0%; Score 1715; DB 2; Length 336; Best Local Similarity 100.0%; Score 1715; DB 2; Length 336; Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVKVKGNGFGRIGLAFRRIQNTVEGVTTRINDLTDPMMLAHLYDTTQGRFDGTV 60

Qy 1 MVVKVKGNGFGRIGLAFRRIQNTVEGVTTRINDLTDPMMLAHLYDTTQGRFDGTV 60

DEGERT 6

OX NCBI_TaxID=11313;

OX [1] _SEQUENCE FROM N.A.

OX RN RP STRAIN=AICC BAA-334 / TIGR4;

OX RC STRAIN=AICC BAA-334 / TIGR4;

OX RX MEDLINE=11357209; PubMed=11463915;

OX RA Tettelin H., Nelson K.B., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapfel E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt T.E., Lottis B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

OX NCBI_TaxID=1307;

OX RN RP "Complete Genome sequence of a virulent isolate of *Streptococcus pneumoniae*." J. Bacteriol. 186: 498-506 (2004).

OX RN [2] _SEQUENCE FROM N.A.

OX RN RP STRAIN=ATCC1133;

OX RC Bergmann S., Hammerschmidt S.;

OX RA "Identification of pneumococcal GAPDH as plasminogen-binding protein." J. Bacteriol. 186: 498-506 (2004).

OX RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

OX RL EMBL; AB007490; AAC76079.1; -.

OX DR EMBL; AJ515822; CAD44376.1; -.

OX PIR; F95235; F95235.

OX HSSP; P00354; 3 GDP.

OX DR TIGR; SP2012; -.

OX DR GO; GO:004365; P:Glyceraldehyde-3-phosphate dehydrogenase (p-); IEA.

OX DR GO; GO:0006096; P:Glycolysis; IEA.

OX DR InterPro; IPR00173; GAPDH-I.

OX DR InterPro; IPR00173; GAP_dhdrogenase.

OX DR Pfam; PF00044; Spdh; 1.

OX DR Pfam; PF02800; Spdh_C; 1.

OX DR Pfam; PF00078; GDPDHGNASE.

OX DR PRINTS; TIGR01534; GAPDH-I.

OX DR PROSITE; PS00071; GAPDH; 1.

OX DR PROSITE; PS00071; GAPDH; 1.

OX DR Oxidoreductase; PS00071; GAPDH; 1.

OX SQ 336 AA; 35825 MW; 1DBB9BA492DCF59 CRC64;

OX SQ 336 AA; 35825 MW; 1DBB9BA492DCF59 CRC64;

OX Query Match 93.1%; Score 1556; DB 2; Length 336;

OX Best Local Similarity 91.1%; Pred. No. 5.4e-99;

OX Matches 306; Conservative 17; Mismatches 13; Indels 0; Gaps 0;

OX Db 1 MVVKVGGFGRIGRLAFRRRIQNYEGVETRINDLTDPMLAHLLKDTDTQGRFDGTYE 60

OX Db 1 MVVKVGGFGRIGRLAFRRRIQNYEGVETRINDLTDPMLAHLLKDTDTQGRFDGTYE 60

OX Qy 61 KEGGFIVNGNFKVSAERDENTIDATDGEIVILEATGFAKKEAERHLHANGAKKVV 120

OX Db 61 KDGGEFVNKGKPVSAERDENTIDATDGEIVILEATGFAKKEAERHLHANGAKKVV 120

OX Qy 121 TAPGNDVTKVYENTHDILDGTETVYISGASCTINCLAPMAKALHDAFGIQKGLMTTHA 180

OX Db 121 TAPGNDVTKVYENTHDILDGTETVYISGASCTINCLAPMAKALHDAFGIQKGLMTTHA 180

OX Qy 181 YTGQMDLDPGRGGDLRARAAGANIVNPNSTGAAKAGIVIPIELNGKLDGAQRVPT 240

OX Db 181 YTGQMDLDPGRGGDLRARAAGANIVNPNSTGAAKAGIVIPIELNGKLDGAQRVPT 240

OX Qy 241 GSVTELVATLDKVSYDEINAMKASNSDFGTYEDPIVSSDTIYGVSYGSFLDATQTKM 300

OX Db 241 GSVTELVATLDKVSYDEINAMKASNSDFGTYEDPIVSSDTIYGVSYGSFLDATQTKM 300

OX Qy 301 EVDGSQLKVKVSYWYDNEMSIATQQLVRLTEYFAKAK 336

OX Db 301 EVDGSQLKVKVSYWYDNEMSIATQQLVRLTEYFAKAK 336

OX Qy 336 AA; 35825 MW; 1DBB9BA492DCF59 CRC64;

OX RN RESULT 7

OX ID Q97N11 PRELIMINARY; PRT; 335 AA.

OX AC 097N11; 01-OCT-2001 (TRIMBLrel. 18, Created)

OX DT 01-OCT-2003 (TRIMBLrel. 18, Last sequence update)

OX DT 01-OCT-2003 (TRIMBLrel. 25, Last annotation update)

OX DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).

OX GS Streptococcus pneumoniae.

OX Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OX Streptococcus.

DT	01-MAR-2003 (TREMBUREL. 23, Created)	DT	01-OCT-2002 (TREMBUREL. 22, Last sequence update)
DT	01-MAR-2003 (TREMBUREL. 23, Last annotation update)	DT	01-OCT-2003 (TREMBUREL. 25, Last annotation update)
DE	Glyceraldehyde 3-phosphate dehydrogenase (Phosphorylating (EC 1.2.1.12).	DE	Glyceraldehyde-3-phosphate dehydrogenase.
DE	Glyceraldehyde 3-phosphate dehydrogenase (Phosphorylating (EC 1.2.1.12).	DE	Glyceraldehyde-3-phosphate dehydrogenase.
GN	Streptococcus pneumoniae (strain ATCC BAA-255 / R6).	OS	Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
NCBI_TaxID	171101;	NCBI_TaxID	1346;
OX		OX	
RN		RN	
SEQUENCE FROM N.A.		SEQUENCE FROM N.A.	
RP		RP	
SEQUENCE FROM N.A.; PubMed=11544234;		SPECIES=S. agalactiae, and S. iniae; STRAIN=ATCC 27541, and 9117;	
RP		RC	
SEQUENCE FROM N.A.; PubMed=11544234;		Fontaine M.C., Perez-Castañ J., Song X.-M., Shelford J., Willison P.J.,	
RP		Potter A.A.;	
RA	Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczaik L.C., Burgett S.,	RA	Immunization of dairy cattle with recombinant GAPC and chimeric CAMP
RA	Dash B., Estrem S.P., Fritz L., Fu D.-J., Fuller W., Geringer C.,	RA	antigens confers protection against heterologous Challenge with
RA	Gilmour R., Glass J.S., Khoa H., Kratt A.R., Lagace R.B.,	RT	Streptococcus uberis.";
RA	LeBlanc D.J., Lee L.N., Lefebvre E.J., Lu J., Matsushima P.,	RL	Submitted (SEP 2001) to the EMBL/GenBank/DBJ databases.
RA	McAuliffe S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,	CC	- SIMILARITY. BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
RA	Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocley P.,	CC	DEHYDROGENASE FAMILY.
RA	Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,	DR	EMBL: AF421902; AAC73770.1; -
RA	Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,	DR	DR: AF421902; AAC73773.1; -
RA	Glass J.I.;	DR	GO: 0004365; P: glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.
RT	"Genome of the bacterium Streptococcus pneumoniae strain R6.";	DR	GO: 0016491; P: oxidoreductase activity; IEA.
RL	J. Bacteriol. 183:5709-5717 (2001).	DR	GO: 0006096; P: glycolysis; IEA.
EMBL; AE008547; AL00658.1;	-	DR	InterPro; IPR00177; GAPDH-I.
DR	PIR: G98099; G98099.	DR	Pfam; PF00044; spdh. 1. _
GO	GO: 0004365; P: glyceraldehyde-3-phosphate dehydrogenase (p. . .); IEA.	DR	PRINTS; PRO0078; GAPDH-GRNASS.
GO	GO: 0006096; P: glycolysis; IEA.	DR	TIGR40153; GAPDH-I.
DR	InterPro; IPR006424; GAPDH-I.	DR	PROSITE; PS00071; GAPDH-I.
DR	InterPro; IPR000177; GAP_dndrogenase.	KW	Oxidoreductase.
DR	Pfam; PF00044; spdh. 1.	SEQUENCE	336 AA; 357/23 MW; ABAB9E14F3ED1111 CRC64;
DR	PRINTS; PRO00078; C3EDPHDRGNASE.	Query Match	92.4%; Score 1584; DB 2; Length 336;
DR	TIGR40153; GAPDH-I.	Best Local Similarity	90.5%; Pred. No. 3.4e-98;
DR	PROSITE; PS00071; GAPDH-I.	Matches	304; Conservative 19; Mismatches 13; Indels 0; Gaps 0;
KW	Complete proteome.		
SEQUENCE	359 AA; 38763 MW; 61EF0375B330B60 CRC64;	Qy	1 MVKVKGINGFGRIGRLAARRQINVEGVETRINDLTDPMMLAHLLKYDTTQGRFDGTYEV
Qy	1 MVKVKGINGFGRIGRLAARRQINVEGVETRINDLTDPMMLAHLLKYDTTQGRFDGTYEV	60	61 KEGGPFENGFKVSAERPDENIDWATGVEVILEATGFFAKKEAEKHLHANGAKVYI
Db	25 MVKVKGINGFGRIGRLAARRQINVEGVETRINDLTDPMMLAHLLKYDTTQGRFDGTYEV	84	61 KEGGPFENGFKVSAERPDENIDWATGVEVILEATGFFAKKEAEKHLHANGAKVYI
Qy	1 MVKVKGINGFGRIGRLAARRQINVEGVETRINDLTDPMMLAHLLKYDTTQGRFDGTYEV	60	61 KEGGPFENGFKVSAERPDENIDWATGVEVILEATGFFAKKEAEKHLHANGAKVYI
Db	61 KEGGPFENGFKVSAERPDENIDWATGVEVILEATGFFAKKEAEKHLHANGAKVYI	120	61 KEGGPFENGFKVSAERPDENIDWATGVEVILEATGFFAKKEAEKHLHANGAKVYI
Db	85 KEGGPFENGFKVSAERPDENIDWATGVEVILEATGFFAKKEAEKHLHANGAKVYI	143	121 TAPGNDVDTKVTVNTHDILDGTETVIGSACSTCNLAPAKALDQFLQKGMLNTIHA
Qy	121 TAPGNDVDTKVTVNTHDILDGTETVIGSACSTCNLAPAKALDQFLQKGMLNTIHA	180	121 TAPGNDVDTKVTVNTHDILDGTETVIGSACSTCNLAPAKALDQFLQKGMLNTIHA
Db	144 TAPGNDVDTKVTVNTHDILDGTETVIGSACSTCNLAPAKALDQFLQKGMLNTIHA	203	121 TAPGNDVDTKVTVNTHDILDGTETVIGSACSTCNLAPAKALDQFLQKGMLNTIHA
Qy	181 YTGDDMLDGPGRGGDLRARRAGANIVPNSTGAAKAGIVIPELNGKLGDGAQRVPVPT	240	181 YTGDDMLDGPGRGGDLRARRAGANIVPNSTGAAKAGIVIPELNGKLGDGAQRVPVPT
Db	204 YTGDDMLDGPGRGGDLRARRAGANIVPNSTGAAKAGIVIPELNGKLGDGAQRVPVPT	263	181 YTGDDMLDGPGRGGDLRARRAGANIVPNSTGAAKAGIVIPELNGKLGDGAQRVPVPT
Qy	241 GSVTELVVLTDKVSYDEINAAMKAASNSFGTETPIVSSDIVGVYGSLSFDATQTKM	300	241 GSVTELVVLTDKVSYDEINAAMKAASNSFGTETPIVSSDIVGVYGSLSFDATQTKM
Db	264 GSVTELVVLTDKVSYDEINAAMKAASNSFGTETPIVSSDIVGVYGSLSFDATQTKM	323	241 GSVTELVVLTDKVSYDEINAAMKAASNSFGTETPIVSSDIVGVYGSLSFDATQTKM
Qy	301 EVDGSQLVVKVYSWYDNEMSYTAQLVRLYFAKIAK	336	301 EVDGSQLVVKVYSWYDNEMSYTAQLVRLYFAKIAK
Db	324 DVDGQLVVKVYSWYDNEMSYTAQLVRLYFAKIAK	359	324 DVDGQLVVKVYSWYDNEMSYTAQLVRLYFAKIAK
RESULT 10		Q8DVV3	PRELIMINARY; PRT; 337 AA.
Q8KHG1		AC	Q8DVV3; PRELIMINARY; PRT; 337 AA.
ID		ID	Q8DVV3; PRELIMINARY; PRT; 337 AA.
AC		AC	Q8DVV3; PRELIMINARY; PRT; 337 AA.
DT	01-MAR-2003 (TREMBUREL. 23, Created)	DT	01-MAR-2003 (TREMBUREL. 23, Last sequence update)
DT	01-MAR-2003 (TREMBUREL. 23, Last sequence update)	DT	01-MAR-2003 (TREMBUREL. 23, Last annotation update)
DT	01-Oct-2003 (TREMBUREL. 25, Last annotation update)	DT	01-Oct-2003 (TREMBUREL. 25, Last annotation update)
DE	Extracellular glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).	DE	Extracellular glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).
GN	GAPC OR SMU-360.	GN	GAPC OR SMU-360.

DR	Pfam; PF00044; Spdh; 1.
DR	Pfam; PF02800; Spdh; C; 1.
DR	PRINTS; PRO0078; G3PDH/DRGNASE;
DR	TIGRFAMS; TIGR01534; GAPDH-1; 1.
DR	PROSITE; PS00071; GAPDH; 1.
DR	Oxidoreductase.
FT	NON_TER 1 1
FT	NON_TER 320 320 AA; 33966 MW; 6FFCC16BBB01E91F0 CRC64;
SQ	SEQUENCE 336 AA; 3626 MW; 52C1F25F3A7E0230 CRC64;
Query Match	91.7%; Score 1572; DB 2; Length 336;
Best Local Similarity	90.2%; Pred. No. 2.2e-97; Indels 0; Gaps 0;
Matches	303; Conservative 18; Mismatches 15; Indels 0; Gaps 0;
Qy	1 MVRKVINGFGRIGRLAFRRIQNEVGVETRINDLDPMLAHLLKYDTQGRFQDGTVKEG 60
Db	1 MVRKVINGFGRIGRLAFRRIQNEVGVETRINDLDPMLAHLLKYDTQGRFQDGTVEL 60
Qy	61 KEGGFYEVNGFGRIGRLAFRRIQNEVGVETRINDLDPMLAHLLKYDTQGRFQDGTV 60
Db	61 KEGGFYEVNGFGRIGRLAFRRIQNEVGVETRINDLDPMLAHLLKYDTQGRFQDGTVL 60
Qy	61 KEGGFYEVNGFGRIGRLAFRRIQNEVGVETRINDLDPMLAHLLKYDTQGRFQDGTV 60
Db	61 KEGGFYEVNGFGRIGRLAFRRIQNEVGVETRINDLDPMLAHLLKYDTQGRFQDGTVL 60
Qy	121 TAPGNDVTKVTFNTNHDLDGTEVTSAGSCTNCLAPMAKALHDARGIQKGLMTTHA 120
Db	121 TAPGNDVTKVTFNTNHDLDGTEVTSAGSCTNCLAPMAKALHDARGIQKGLMTTHA 120
Qy	181 YTQDMQMLDGPHEGDLARRAGANTIPNSTAGAAAGLVIEBLNGLQDGAAQRVPPT 240
Db	181 YTQDMQMLDGPHEGDLARRAGANTIPNSTAGAAAGLVIEBLNGLQDGAAQRVPPT 240
Qy	121 TAPGNDVTKVTFNTNHDLDGTEVTSAGSCTNCLAPMAKALHDARGIQKGLMTTHA 180
Db	121 TAPGNDVTKVTFNTNHDLDGTEVTSAGSCTNCLAPMAKALHDARGIQKGLMTTHA 180
Qy	181 YTQDMQMLDGPHEGDLARRAGANTIPNSTAGAAAGLVIEBLNGLQDGAAQRVPPT 240
Db	181 YTQDMQMLDGPHEGDLARRAGANTIPNSTAGAAAGLVIEBLNGLQDGAAQRVPPT 240
Qy	241 GSYVTELVVTLDKNVSVDENAAKASNDSEFGTYEDPVISSDIVGVSYGSLSFATQKVM 300
Db	241 GSYVTELVVTLDKNVSVDENAAKASNDSEFGTYEDPVISSDIVGVSYGSLSFATQKVL 300
Qy	301 EVDGSOLVKVSYDNEMSYTQSVLRTLEYFAKIAK 336
Db	301 DVDGKOLVKVSYDNEMSYTQSVLRTLEYFAKIAK 336
RESULT 14	Q9AJT7 PRELIMINARY; PRT; 309 AA.
Q9AJT7	AC Q9AJT7 PRELIMINARY; PRT; 309 AA.
AC	Q9AJT7; 01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12).
DS	(Fragment).
DS	Streptococcus pneumoniae.
DS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
DS	streptococcus.
DS	NCBI_TaxID=1313;
RN	RN SEQUENCE FROM N.A.
RC	RC STRAIN=Clinical isolate;
RA	Amezaga M.R.; Carter P.E.; Cash P.; McKenzie H.;
RT	RT Sequence variation in ref (A) and gap genes in M-phenotype erythromycin resistant Streptococcus pneumoniae.;
RL	RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC	CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FAMILY.
DR	DR EMBL: AJ292048; CAC27448-1; -
DR	DR HSSP: P0362; 1SD;
DR	DR GO:0004465; P:glyceraldehyde-3-phosphate dehydrogenase activity; IEA.
DR	DR GO; GO:0016491; F:oxido-reductase activity; IEA.
DR	DR PRINTS; PRO0078; G3PDH/DRGNASE.
DR	DR TIGRFAMS; TIGR01534; GAPDH-1; 1.
DR	DR InterPro; IPR006424; GAPDH-1.
DR	DR GO; GO:004465; F:glyceraldehyde-3-phosphate dehydrogenase (p. . . IEA.
DR	DR GO; GO:0016491; F:oxido-reductase activity; IEA.
DR	DR GO; GO:000696; P:glycolysis; IEA.
DR	DR GO; GO:000696; P:glycolysis; IEA.
DR	DR InterPro; IPR000173; GAP chdrogenase.
DR	DR PROSITE; PS00071; GAPDH; 1.
DR	DR PRINTS; PRO0078; G3PDH/DRGNASE.
DR	DR TIGRFAMS; TIGR01534; GAPDH-1; 1.

DR PROSITE; PS00071; GARDH; 1.
 KW Oxidoreductase; .
 FT 1
 NON TER 309 309
 SQ SEQUENCE 309 AA; 32930 MW; 89E45CC3BEA6A0528 CRC64;
 Query Match 85.6%; Score 1468.5; DB 2; Length 309;
 Best Local Similarity 91.9%; Pred. No. 1.7e-90; Indels 1; Gaps 1;
 Matches 285; Conservative 12; Mismatches 13; N mismatches 12; Indels 1; Gaps 1;
 Qy 9 GFGGRIGRLAARRQIVNVEGVETRINDLDPNMLAHLKXDTTQGRFDGTVKEGGFENV 68
 Db 1 GFGGRIGRLAARRQIVNVEGVETRINDLDPNMLAHLKXDTTQGRFDGTVKEGGFENV 60
 Qy 69 GNFIIKVSAAEDPENIDWATGVEIVLEATFFAKKEAERKHLHANGAKKVITAPGGNDV 128
 Db 61 GKFIIKVSAAEDPENIDWATGVEIVLEATFFAKKEAERKHL-KGGAKKVVITAPGGNDV 119
 Qy 129 KTVVVENTNHDILDGETVIGASCTTNCAPMAKALHDAGIQKGLMTTHAYTGDQML 188
 Db 120 KTVVVENTNHDILDGETVIGASCTTNCAPMAKALQDFGKQVTEGLMTTHAYTGDQML 179
 Qy 129 DGPGRGGDLRARAAGANITPNSTGAAKAIGLVPELNKGKDQDFGKQVTEGLMTTHAYTGDQML 188
 Db 120 DGPGRGGDLRARAAGANITPNSTGAAKAIGLVPELNKGKDQDFGKQVTEGLMTTHAYTGDQML 179
 Qy 189 DGPGRGGDLRARAAGANITPNSTGAAKAIGLVPELNKGKDQDFGKQVTEGLMTTHAYTGDQML 239
 Db 180 DGPGRGGDLRARAAGANITPNSTGAAKAIGLVPELNKGKDQDFGKQVTEGLMTTHAYTGDQML 239
 Qy 249 TLDKQNSVDEINAAMKAASNDSFQYTEDPIVSSD1IVGVSYGSLSLFDATOKYMEVDGSQLV 308
 Db 240 VLEKNTVDEINAAMKAASNESYGTEDPIVSSD1IVGMSYGSLSLFDATOKVLDVDGKLV 299
 Qy 309 KVVSVDNEM 318
 Db 300 KVVSVDNEM 309
 Search completed: May 11, 2004, 16:49:18
 Job time : 52 secs

RESULT 15
 Q9AQT9 PRELIMINARY: PRT: 309 AA.
 ID Q9AQT9
 AC 09AQT9;
 DT 01-JUN-2001 (TREMBUREL 17, Created)
 DT 01-JUN-2001 (TREMBUREL 17, Last sequence update)
 DT 01-OCT-2003 (TREMBUREL 25, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
 DE (Fragment).
 GN GAP.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 Streptococcus.
 OC NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=clinical isolate.
 RA Amezaga M.R., Carter P.E., Cash P., McKenzie H.;
 "Sequence variation in m (A) and gap genes in M-phenotype
 erythromycin resistant Streptococcus pneumoniae";
 Submitted (JAN 2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
 DEHYDROGENASE FAMILY.
 EMBL: AJ292046; CAC27446_1; -.
 DR HSSP; P00362; Igdl.
 DR GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:000696; P:glycolysis; IEA.
 DR Int-Pro; IPR006424; GAPDH-I.
 DR InterPro; IPR000173; GAP_dhydrogenase.
 DR Pfam; PF02800; Spdh_C.
 DR Pfam; PF02800; Spdh_C.
 PRINTS; PRO0078; G3DHDRONASE.
 TIGRFAM; TIG01534; GARDH-I; 1.
 DR PROSITE; PS0001; GARDH-I.
 KW Oxidoreductase.
 FT NON TER 1
 FT NON_TER 309 309 1
 FT

GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2004, 16:49:42 ; Search time 48 Seconds

(without alignments)

1942.967 Million cell updates/sec

Title: US-10-650-369-12

Perfect score: 1715

Sequence: 1 MIVVKGINGRGRIGRIGLAFR.....EMSYTAQLVRLTLEYFAKTAK 336

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:/*
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11: /cgn2_6/ptodata/2/pubpa/US09C_PUBCOMB.pep:/*
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18: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUBCOMB.pep:/*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	100.0	336	9	US-09-878-766A-12	Sequence 12, Appl
2	100.0	336	10	US-09-878-781-4	Sequence 4, Appl
3	100.0	336	12	US-10-650-369-12	Sequence 12, Appl
4	100.0	336	14	US-10-134-297-4	Sequence 4, Appl
5	99.9	336	12	US-10-282-122A-74379	Sequence 74379, A
6	98.5	335	10	US-09-878-781-14	Sequence 14, Appl
7	96.6	448	12	US-10-650-369-22	Sequence 22, Appl
8	96.5	448	12	US-10-650-369-22	Sequence 22, Appl
9	94.3	336	9	US-09-878-766A-16	Sequence 16, Appl
10	94.3	336	10	US-09-878-781-8	Sequence 8, Appl
11	94.3	336	12	US-10-650-369-16	Sequence 16, Appl
12	94.3	336	14	US-10-134-297-8	Sequence 8, Appl
13	93.9	336	10	US-09-878-781-16	Sequence 16, Appl
14	93.4	336	10	US-09-878-781-14	Sequence 14, Appl
15	93.4	336	10	US-09-878-781-6	Sequence 6, Appl

Sequence 14, Appl
Sequence 6, Appl
Sequence 13169, A
Sequence 74186, A
Sequence 13583, A
Sequence 20, Appl
Sequence 12, Appl
Sequence 20, Appl
Sequence 12, Appl
Sequence 7254, A
Sequence 18, Appl
Sequence 10, Appl
Sequence 18, Appl
Sequence 10, Appl
Sequence 54, Appl
Sequence 18342, A
Sequence 10847, A
Sequence 57294, A
Sequence 53466, A
Sequence 60492, A
Sequence 51519, A
Sequence 7134, A
Sequence 65661, A
Sequence 65601, A
Sequence 70890, A
Sequence 12540, A
Sequence 43397, A
Sequence 56828, A

ALIGNMENTS

RESULT 1

US-09-878-766A-12

; Sequence 12, Application US/09878766A
; General Information:
; Applicant: Pottor, Andrew A.
; Applicant: Perez-Casal, Jose
; Applicant: Fontaine, Michael
; Title of Invention: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
; Title of Invention: AGAINST STREPTOCOCCUS INFECTION
; File Reference: 9000-0057
; Current Application Number: US/09-878-766A
; Current Filing Date: 2001-09-10
; Number of SEQ ID NOS: 22
; SEQ ID NO 12
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Streptococcus dysgalactiae

US-09-878-766A-12

Query Match 100.0% ; Score 1715; DB 9; Length 336;
Best Local Similarity 100.0% ; Pred No. 3 1e-154;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVKVINGGRIGRIGLAFRIGVQEVTRINLTDPMMLAHILKYDTTQGRDGTVEV 60
Db 1 MVVKVINGGRIGRIGLAFRIGVQEVTRINLTDPMMLAHILKYDTTQGRDGTVEV 60
Qy 61 KEGGPBVNGNPKVSAERDPEINTDWTGVEVILEATGFRAKKEAAEKLHANGAKVVI 120
Db 61 KEGGPBVNGNPKVSAERDPEINTDWTGVEVILEATGFRAKKEAAEKLHANGAKVVI 120

RESULT 2
 US-09-878-781-4
 Sequence 4, Application US/09878781
 Publication No. US20030082781A1.

GENERAL INFORMATION:
 APPLICANT: Bolton, Alexandra J.
 APPLICANT: Perez-Casal, Jose
 APPLICANT: Fontaine, Michael A.
 APPLICANT: Potter, Andrew A.

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
 FILE REFERENCE: 9000-00555
 CURRENT APPLICATION NUMBER: US/09/878,781
 CURRENT FILING DATE: 2002-09-10
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 4
 LENGTH: 336
 TYPE: PRT
 ORGANISM: Streptococcus dysgalactiae

US-09-878-781-4
 Query Match 100.0%; Score 1715; DB 12; Length 336;
 Best Local Similarity 100.0%; Pred. No. 3.1e-154; Mismatches 0; Indels 0; Gaps 0;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVKVINGFGRIGLAFRRIONVEGVETRINDLTDPMLAHILKYDTTQGRFDGTVEV 60
 Db 1 MVVKVINGFGRIGLAFRRIONVEGVETRINDLTDPMLAHILKYDTTQGRFDGTVEV 60
 Qy 61 KEGGFEVNGNFIKVSaERDENIDATDGVIEVLEATGFAKEAEXHLHANGAKVYI 120
 Db 61 KEGGFEVNGNFIKVSaERDENIDATDGVIEVLEATGFAKEAEXHLHANGAKVYI 120
 Qy 121 TAPGNDVKTIVFVNTHDILDGTETVVISGASCTINCLAPMAKALHDAGFQIKGLMTTHA 180
 Db 121 TAPGNDVKTIVFVNTHDILDGTETVVISGASCTINCLAPMAKALHDAGFQIKGLMTTHA 180
 Qy 181 YTGDQMLDGPHRGDLRARRAGANIVNSTGAKAISVPLNGKLDAAQRPVPT 240
 Db 181 YTGDQMLDGPHRGDLRARRAGANIVNSTGAKAISVPLNGKLDAAQRPVPT 240
 Qy 241 GSVTELVTLDKNSVDEINAMKAANSFEGYEDPIVSSDIVGYSGLFDATQTKM 300
 Db 241 GSVTELVTLDKNSVDEINAMKAANSFEGYEDPIVSSDIVGYSGLFDATQTKM 300
 RESULT 4
 US-10-134-297-4
 Sequence 4, Application US/10134297
 Publication No. US20030165524A1.

GENERAL INFORMATION:
 APPLICANT: Bolton, Alexandra J.
 APPLICANT: Perez-Casal, Jose
 APPLICANT: Fontaine, Michael A.
 APPLICANT: Potter, Andrew A.

TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
 TITLE OF INVENTION: STREPTOCOCCUS INFECTION

FILE REFERENCE: 9000-00555-00
 CURRENT APPLICATION NUMBER: US/10/134,297
 CURRENT FILING DATE: 2002-04-26
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 4
 LENGTH: 336
 TYPE: PRT
 ORGANISM: Streptococcus dysgalactiae

US-10-134-297-4
 Query Match 100.0%; Score 1715; DB 14; Length 336;
 Best Local Similarity 100.0%; Pred. No. 3.1e-154; Mismatches 0; Indels 0; Gaps 0;
 Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVKVINGFGRIGLAFRRIONVEGVETRINDLTDPMLAHILKYDTTQGRFDGTVEV 60
 Db 1 MVVKVINGFGRIGLAFRRIONVEGVETRINDLTDPMLAHILKYDTTQGRFDGTVEV 60
 Qy 61 KEGGFEVNGNFIKVSaERDENIDATDGVIEVLEATGFAKEAEXHLHANGAKVYI 120

RESULT 5
US-10-282-122A-74379
; Sequence 74379, Application US-10282122A.
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangshu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Hasselbeck, Robert
; APPLICANT: Malone, Cheryl
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Travick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forryth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELIGRA.03A
; CURRENT APPLICATION NUMBER: US-10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-3
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-05-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/267,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent-in version 3.1
; SEQ ID NO: 74379
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
; US-10-282-122A-74379

Qy 61 KEGGFEYNGNFKVSERDPENIDWATGVEIVLAKKAGKVVV 120
Db 121 TAPGNDYKTVVNTNHDLDGTETVSGASCTTCNCLAPMAKALHDAGIQKGLMTTHA 180
Qy 121 TAPGNDYKTVVNTNHDLDGTETVSGASCTTCNCLAPMAKALHDAGIQKGLMTTHA 180
Db 181 YTGDQMLDGPGRGDLRARAAGAANTIVNSTGAAKAGLVIPELNGKLDAQAQRYVPT 240
Qy 181 YTGDQMLDGPGRGDLRARAAGAANTIVNSTGAAKAGLVIPELNGKLDAQAQRYVPT 240
Db 181 YTGDQMLDGPGRGDLRARAAGAANTIVNSTGAAKAGLVIPELNGKLDAQAQRYVPT 240
Qy 241 GSVTELVTLDKNVSDTEINAAMKAASNSDSEGYTEDPIVSSDIVGVSYGSLEDATQTKM 300
Db 241 GSVTELVTLDKNVSDTEINAAMKAASNSDSEGYTEDPIVSSDIVGVSYGSLEDATQTKM 300
Qy 301 EVDSQQLVKVSWDNEMSYAQLVRLTEYFAKIAK 336
Db 301 EVDGSQQLVKVSWDNEMSYAQLVRLTEYFAKIAK 336

RESULT 6
US-09-878-781-14
; Sequence 14, Application US-09878781
; Publication No. US20030082781A1
; GENERAL INFORMATION:
; APPLICANT: Bolton, Alexandra J.
; APPLICANT: Perez-Casal, Jose
; APPLICANT: Fontaine, Michael
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
; TITLE OF INVENTION: STREPTOCOCCUS INFECTION
; FILE REFERENCE: 900-0055
; CURRENT APPLICATION NUMBER: US-09/878,781
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 14
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SpyGapC
; OTHER INFORMATION: protein
; US-09-878-781-14

Query Match 1 MVVKVINGFGRIGRAFRRIQVNGVEVTRINDLTDPMNLALIHKYDTTQGRFDGTVV 60
Best Local Similarity 1 MVVKVINGFGRIGRAFRRIQVNGVEVTRINDLTDPMNLALIHKYDTTQGRFDGTVV 60
Matches 1 Indels 1; Gaps 1;
Qy 61 KEGGFEYNGNFKVSERDPENIDWATGVEIVLAKKAGKVVV 120
Db 121 TAPGNDYKTVVNTNHDLDGTETVSGASCTTCNCLAPMAKALHDAGIQKGLMTTHA 180
Qy 181 YTGDQMLDGPGRGDLRARAAGAANTIVNSTGAAKAGLVIPELNGKLDAQAQRYVPT 240
Db 180 YTGDQMLDGPGRGDLRARAAGAANTIVNSTGAAKAGLVIPELNGKLDAQAQRYVPT 239
Qy 241 GSVTELVTLDKNVSDTEINAAMKAASNSDSEGYTEDPIVSSDIVGVSYGSLEDATQTKM 300

Query Match 1 MVVKVINGFGRIGRAFRRIQVNGVEVTRINDLTDPMNLALIHKYDTTQGRFDGTVV 60
Best Local Similarity 1 MVVKVINGFGRIGRAFRRIQVNGVEVTRINDLTDPMNLALIHKYDTTQGRFDGTVV 60
Matches 1 Indels 1; Gaps 1;
Qy 61 KEGGFEYNGNFKVSERDPENIDWATGVEIVLAKKAGKVVV 120
Db 121 TAPGNDYKTVVNTNHDLDGTETVSGASCTTCNCLAPMAKALHDAGIQKGLMTTHA 180
Qy 181 YTGDQMLDGPGRGDLRARAAGAANTIVNSTGAAKAGLVIPELNGKLDAQAQRYVPT 240
Db 180 YTGDQMLDGPGRGDLRARAAGAANTIVNSTGAAKAGLVIPELNGKLDAQAQRYVPT 239
Qy 241 GSVTELVTLDKNVSDTEINAAMKAASNSDSEGYTEDPIVSSDIVGVSYGSLEDATQTKM 300

APPLICANT: Potter, Andrew A.
 TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
 STREPTOCOCCUS INFECTION
 FILE REFERENCE: 9000-0055.0
 CURRENT APPLICATION NUMBER: US/10/134,297
 CURRENT FILING DATE: 2002-04-26
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 8
 LENGTH: 336
 TYPE: PRT
 ORGANISM: Streptococcus uberis
 US-10-134-297-8

Query Match 94.3%; Score 1618; DB 14; Length 336;
 Best Local Similarity 92.9%; Pred. No. 5.1e-145; Indels 0; Gaps 0;
 Matches 312; Conservative 15; Mismatches 9;

Qy 1 MVVKVINGFCRIGLAFKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Db 1 MVVKVINGFCRIGLAFKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Qy 61 KEGGFVNGFPIKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Db 61 KEGGFVNGFPIKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Qy 121 TAPGNDVKTIVFNTNHDLDGTETVVISGASCTNCLAPMAKALQDNFGVKQGLMTIHA 180
 Db 121 TAPGNDVKTIVFNTNHDLDGTETVVISGASCTNCLAPMAKALQDNFGVKQGLMTIHA 180
 Qy 181 YTGDQMLDGFHRSGLRARRAGAANTIVNSTGAKAIGLVIPBLNGKDGAQRVYFPT 240
 Db 181 YTGDQMLDGFHRSGLRARRAGAANTIVNSTGAKAIGLVIPBLNGKDGAQRVYFPT 240
 Qy 241 GSVTEIVVTLDKNSVDEINAMKAANSFGTEDPIVSSD1VGSLSLFDATQTKV 300
 Db 241 GSVTEIVVTLDKNSVDEINAMKAANSFGTEDPIVSSD1VGSLSLFDATQTKV 300
 Qy 301 EVDGSQLVKVWSWDEMSYTAQLVRLTEYFAKIAK 336
 Db 301 EVDGSQLVKVWSWDEMSYTAQLVRLTEYFAKIAK 336

RESULT 14
 US-09-878-766A-14
 / Sequence 14, Application US/09878766A
 / Patent No. US2002044928A1
 / GENERAL INFORMATION:
 / APPLICANT: Potter, Andrew A.
 / ATTORNEY: Perez-Casal, Jose
 / ATTORNEY: Fontaine, Michael
 / TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
 / TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION
 / FILE REFERENCE: 9000-0057
 / CURRENT FILING DATE: 2001-09-10
 / NUMBER OF SEQ ID NOS: 22
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO: 14
 / LENGTH: 336
 / TYPE: PRT
 / ORGANISM: Streptococcus agalactiae
 US-09-878-766A-14

Query Match 93.4%; Score 1602; DB 9; Length 336;
 Best Local Similarity 91.7%; Pred. No. 1.7e-143;
 Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MVVKVINGFCRIGLAFKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Db 1 MVVKVINGFCRIGLAFKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Qy 61 KEGGFVNGFPIKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Db 61 KEGGFVNGFPIKSAERDPEINWVTRINDLTDPMMLAHLLKDTQGRFDGTVVE 60
 Qy 121 TAPGNDVKTIVFNTNHDLDGTETVVISGASCTNCLAPMAKALHAFQIQLMTIHA 180
 Db 121 TAPGNDVKTIVFNTNHDLDGTETVVISGASCTNCLAPMAKALHAFQIQLMTIHA 180
 Qy 181 YTGDQMLDGFHRSGLRARRAGAANTIVNSTGAKAIGLVIPBLNGKDGAQRVYFPT 240
 Db 181 YTGDQMLDGFHRSGLRARRAGAANTIVNSTGAKAIGLVIPBLNGKDGAQRVYFPT 240
 Qy 241 GSVTEIVVTLDKNSVDEINAMKAANSFGTEDPIVSSD1VGSLSLFDATQTKV 300
 Db 241 GSVTEIVVTLDKNSVDEINAMKAANSFGTEDPIVSSD1VGSLSLFDATQTKV 300
 Qy 301 EVDGSQLVKVWSWDEMSYTAQLVRLTEYFAKIAK 336
 Db 301 EVDGSQLVKVWSWDEMSYTAQLVRLTEYFAKIAK 336

RESULT 13
 US-09-878-781-16
 / Sequence 16, Application US/09878781
 / Publication No. US20030082781A1
 / GENERAL INFORMATION:
 / APPLICANT: Bolton, Alexandra J.
 / ATTORNEY: Perez-Casal, Jose
 / ATTORNEY: Fontaine, Michael
 / APPLICANT: Potter, Andrew A.
 / TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
 / TITLE OF INVENTION: STREPTOCOCCUS INFECTION
 / FILE REFERENCE: 9000-0055
 / CURRENT APPLICATION NUMBER: US/09/878,781
 / CURRENT FILING DATE: 2002-09-10
 / NUMBER OF SEQ ID NOS: 18
 / SOFTWARE: Patentin Ver. 2.0
 / SEQ ID NO: 16
 / LENGTH: 336
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: SeqGapC
 / OTHER INFORMATION: protein
 US-09-878-781-16

Query Match 93.9%; Score 1611; DB 10; Length 336;
 Best Local Similarity 95.2%; Pred. No. 2.3e-144;
 Matches 320; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

RESULT 15
 US-09-878-781-6
 Sequence 6, Application US/09878781
 Publication No. US20030082781A1
 GENERAL INFORMATION:
 APPLICANT: Bolton, Alexandra J.
 APPLICANT: Perez-Casal, Jose
 APPLICANT: Fontaine, Michael
 APPLICANT: Potter, Andrew A.
 TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST
 STREPTOCOCCUS INFECTION
 FILE REFERENCE: 900-0055
 CURRENT APPLICATION NUMBER: US/09/878, 781
 CURRENT FILING DATE: 2002-09-10
 NUMBER OF SEQ ID NOS: 18
 SEQ ID NO 6
 SOFTWARE: Patentin Ver. 2.0
 LENGTH: 336
 TYPE: PRT
 ORGANISM: Streptococcus agalactiae
 US-09-878-781-6

Query Match 93.4%; Score 1602; DB 10; Length 336;
 Best Local Similarity 91.7%; Pred. No. 1.76-143; Indels 0; Gaps 0;
 Matches 308; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
 Qy 1 MVVKYGINFGGRIGRLAARRIQLVYEVTRINLDTPNMLAHLKLYDTTQGRFDGVVEV 60
 Db 1 MVVKYGINFGGRIGRLAARRIQLVYEVTRINLDTPNMLAHLKLYDTTQGRFDGVVEV 60
 Qy 61 KEGGFPEVNGNFIKVAERDPEENIDWATDGVETIVLEATGFFAKKAAEKKHLHANGAKKVVI 120
 Db 61 KEGGFPEVNGNFIKVAERDPEENIDWATDGVETIVLEATGFFAKKAAEKKHLHANGAKKVVI 120
 Qy 121 TAPGNDVYCVVVENTNHDLDGTETVVISASCTNCLAMAKALHDAGIQCLMLTTIHA 180
 Db 121 TAPGNDVYCVVVENTNHDLDGTETVVISASCTNCLAMAKALQDNFGVKQCLMLTTIHA 180
 Qy 181 YTGDOMILQPHRGDILRARRAGANIVNSTGAKAIGLVIPELNGKLDDGAQQRVVP 240
 Db 181 YTGDOMILQPHRGDILRARRAGANIVNSTGAKAIGLVIPELNGKLDDGAQQRVVP 240
 Qy 241 GSVTPELVVTDKXVSDEINAMKAASNDSFGYTEDPIVSSDIVGVSYGSFLDATOTKVM 300
 Db 241 GSVTPELVVTDKXVSDEINAMKAASNDSFGYTEDPIVSSDIVGVSYGSFLDATOTKVM 300
 Qy 301 EVDGSQLVKVSWDNEMSYTAOLVRLTYYFAKIAK 336
 Db 301 TVDGNQLVKVSWDNEMSYTSQLVRLTYYFAKIAK 336

Search completed: May 11, 2004, 16:55:20
 Job time : 49 secs